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U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1781

U.S. APPLICATION NO. (If known, see 37 CFR § 1.5)

09/673840

INTERNATIONAL APPLICATION NO PCT/DE99/01163	INTERNATIONAL FILING DATE 15 April 1999	PRIORITY DATE CLAIMED 21 April 1998
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TITLE OF INVENTION

HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BLADDER TISSUE

APPLICANT(S) FOR DO/EO/US

SPECHT, Thomas, et al.

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
 2. This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371.
 3. This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
 4. A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
 5. A copy of the International Application as filed (35 U.S.C. §371(c)(2))
 - a. is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. has been transmitted by the International Bureau.
 - c. is not required, as the application was filed in the United States Receiving Office (RO/US)
 6. A translation of the International Application into English (35 U.S.C. §371(c)(2)).
 7. A copy of the International Search Report (PCT/ISA/210).
 8. Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
 - a. are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. have been transmitted by the International Bureau.
 - c. have not been made; however, the time limit for making such amendments has NOT expired.
 - d. have not been made and will not be made.
 9. A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
 10. An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
 11. A copy of the International Preliminary Examination Report (PCT/IPEA/409).
 12. A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).
- Items 13. to 19. below concern document(s) or information included:**
13. An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
 14. An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included
 15. A **FIRST** preliminary amendment.
 - A **SECOND** or **SUBSEQUENT** preliminary amendment.
 16. A substitute specification.
 17. A change of power of attorney and/or address letter.
 18. Certificate of Mailing by Express Mail
 19. Other items or information:

Sequence Listing with disk

COPY

U.S. APPLICATION NO. <i>09/673840</i>	INTERNATIONAL APPLICATION NO PCT/DE99/01163	ATTORNEY'S DOCKET NUMBER SCH 1781																
<input checked="" type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR §1.492 (a) (1) - (5)): Search Report has been prepared by the EPO or JPO..... \$860.00 International preliminary examination fee paid to USPTO (37 CFR §1.482)..... \$690.00 No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2))..... \$710.00 Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO..... \$1,000.00 International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4)..... \$100.00		CALCULATIONS PTO USE ONLY																
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Surcharge of \$130.00 for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)).		<input type="checkbox"/> 20 <input type="checkbox"/> 30 \$0.00																
<table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th>CLAIMS</th> <th>NUMBER FILED</th> <th>NUMBER EXTRA</th> <th>RATE</th> </tr> </thead> <tbody> <tr> <td>Total claims</td> <td>- 20 =</td> <td>0</td> <td>x \$ 18.00</td> </tr> <tr> <td>Independent claims</td> <td>- 3 =</td> <td>0</td> <td>x \$ 80.00</td> </tr> <tr> <td colspan="2">MULTIPLE DEPENDENT CLAIM(S) (if applicable)</td> <td></td> <td>+ \$ 270.00</td> </tr> </tbody> </table>		CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE	Total claims	- 20 =	0	x \$ 18.00	Independent claims	- 3 =	0	x \$ 80.00	MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$ 270.00	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE															
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MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$ 270.00															
TOTAL OF ABOVE CALCULATIONS =		\$860.00																
Reduction of $\frac{1}{2}$ for filing by small entity, if applicable. A Verified Small Entity Statement must also be filed (Note 37 C.F.R. §§ 1.9, 1.27, 1.28).																		
SUBTOTAL =		\$0.00																
Processing fee of \$130.00 for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)).																		
TOTAL NATIONAL FEE =		\$860.00																
Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property.																		
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a. <input checked="" type="checkbox"/> A check in the amount of <u>\$860.00</u> to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. <u>13-3402</u> in the amount of <u>\$</u> to cover the above fees. A duplicate copy of this sheet is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>13-3402</u> . A duplicate copy of this sheet is enclosed.																		
NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.157(a) or (b)) must be filed and granted to restore the application to pending status.																		
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 SIGNATURE																		
Harry B. Shubin NAME																		
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IN THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

International Application No. : PCT/DE99/01163
International Filing Date : 15 APRIL 1999
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Deposit Date U.S. Nat'l Phase : 23 OCTOBER 2000
Priority Date(s) Claimed : 21 APRIL 1998
Applicant(s) : SPECHT, Thomas, et al.

Title: HUMAN NUCLEIC ACID SEQUENCES OF NORMAL BLADDER TISSUE

PRELIMINARY AMENDMENT

Commissioner for Patents
Box PCT
Washington, D.C. 20231

Sir:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend as follows:

IN THE CLAIMS:

3. (Amended) Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2, characterized in that they are expressed elevated in normal bladder tissue.

4. (Amended) BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for use as vehicles for gene transfer.

5. (Amended) A nucleic acid sequence according to claim 1, wherein it has 90% homology to a human nucleic acid sequence.

6. (Amended) A nucleic acid sequence according to claim 1, wherein it has 95% homology to a human nucleic acid sequence.

7. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claim 1, in such a sufficient amount that they hybridize with the sequences according to claim 1.

8. (Amended) A nucleic acid sequence according to claim 1, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. (Amended) A nucleic acid sequence according to claim 1, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. (Amended) A nucleic acid sequence according to claim 1, which codes at least one partial sequence of a bioactive polypeptide.

11. (Amended) An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 1, together with at least one control or regulatory sequence.

13. (Amended) An expression cassette according to claim 11, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. (Amended) Use of nucleic acid sequences according to claim 1 for producing full-length genes.

16. (Amended) Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to claim 1.

18. (Amended) Host cell according to claim 16, wherein the prokaryotic cell system is *E. coli*, and the eukaryotic cell system is an animal, human or yeast cell system.

19. (Amended) A process for producing a polypeptide or a fragment, wherein the host cells according to claim 16 are cultivated.

27. (Amended) Use of polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as tools for finding active ingredients against the bladder tumor.

28. (Amended) Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for expression of polypeptides that can be used as tools for finding active ingredients against the bladder tumor.

29. (Amended) Use of nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 in sense or antisense form.

30. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as pharmaceutical agents in gene therapy for treatment of the bladder tumor.

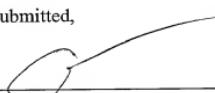
31. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 for the production of a pharmaceutical agent for treatment of the bladder tumor.

32. (Amended) Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431 of claim 23.
33. (Amended) A nucleic acid sequence according to claim 1, wherein it is a genomic sequence.
34. (Amended) A nucleic acid sequence according to claim 1, wherein it is an mRNA sequence.
35. (Amended) Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403 of claim 2.
38. (Amended) A nucleic acid sequence according to claim 1, wherein the size of the fragment has a length of at least 300 to 3500 bp.

REMARKS

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

Claims 3-11, 13-14, 16, 18-19, 27-35 and 38 have been amended as follows:

3. (Amended) Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2, characterized in that they are expressed elevated in normal bladder tissue.
4. (Amended) BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for use as vehicles for gene transfer.
5. (Amended) A nucleic acid sequence according to claimsclaim 1-to-4, wherein it has 90% homology to a human nucleic acid sequence.
6. (Amended) A nucleic acid sequence according to claimsclaim 1-to-4, wherein it has %95% homology to a human nucleic acid sequence.
7. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claimsclaim 1-to-6, in such a sufficient amount that they hybridize with the sequences according to claimsclaim 1-to-6.
8. (Amended) A nucleic acid sequence according to claimsclaim 1-to-7, wherein the size of the fragment has a length of at least 50 to 4500 bp.
9. (Amended) A nucleic acid sequence according to claimsclaim 1-to-7, wherein the size of the fragment has a length of at least 50 to 4000 bp.
10. (Amended) A nucleic acid sequence according to one of claimsclaim 1-to-9, which codes at least one partial sequence of a bioactive polypeptide.
11. (Amended) An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claimsclaim 1-to-9, together with at least one control or regulatory sequence.

13. (Amended) An expression cassette according to ~~one of claims~~claim 11-and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. (Amended) Use of nucleic acid sequences according to ~~claims~~claim 1 to 10 for producing full-length genes.

16. (Amended) Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to ~~one of claims~~claim 1 to 10.

18. (Amended) Host cell according to ~~one of claims~~claim 16 or 17, wherein the prokaryotic cell system is E. coli, and the eukaryotic cell system is an animal, human or yeast cell system.

19. (Amended) A process for producing a polypeptide or a fragment, wherein the host cells according to ~~claims~~claim 16 to 18 are cultivated.

27. (Amended) Use of polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as tools for finding active ingredients against the bladder tumor.

28. (Amended) Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for expression of polypeptides that can be used as tools for finding active ingredients against the bladder tumor.

29. (Amended) Use of nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 in sense or antisense form.

30. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as pharmaceutical agents in gene therapy for treatment of the bladder tumor.

31. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 for the production of a pharmaceutical agent for treatment of the bladder tumor.

32. (Amended) Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431 of claim 23.

33. (Amended) A nucleic acid sequence according to claimsclaim 1-to-10, wherein it is a genomic sequence.

34. (Amended) A nucleic acid sequence according to claimsclaim 1-to-10, wherein it is an mRNA sequence.

35. (Amended) Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403 of claim 2.

38. (Amended) A nucleic acid sequence according to claimsclaim 1-to-7, wherein the size of the fragment has a length of at least 300 to 3500 bp.

Human Nucleic Acid Sequences from Normal Bladder Tissue

The invention relates to human nucleic acid sequences from normal bladder tissue, which code for gene products or portions thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death by cancer is the bladder tumor, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation.

Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this possibility of error can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403, which play a role as candidate genes in the bladder tumor, have now been found.

Nucleic acid sequences Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, and 391-403 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a portion thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, and 391-403,
 - b) an allelic variation of the nucleic acid sequences named under a)
- or
- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, and 391-403 or a complementary or

allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID Nos. 1-127 and 391-403, which are expressed elevated in the normal bladder tissue.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-127 and 391-403.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-127 and 391-403 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs, φX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), 2. eukaryotic,

such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

Control or regulatory sequences are defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P_R, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as *E. coli* or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides, according to the sequence protocols Seq. ID Nos. 128-390 and 404-431.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq ID Nos. 128-390 and 404-431 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-127 and 391-403 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The polypeptides of sequences Seq. ID Nos. 128-390 and 404-431 according to the invention can also be used as tools for finding active ingredients against the bladder tumor, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 for expression of polypeptides, which can be used as tools for finding active ingredients against the bladder tumor.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 as pharmaceutical agents in the gene therapy for treatment of bladder tumors or for the production of a pharmaceutical agent for treatment of bladder tumors.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained

from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences) Seq. ID Nos. 1-127 and 391-403, genomic BAC-, PAC- and cosmid libraries are screened, and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes, and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 for use as vehicles for gene transfer.

Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:
mRNA, partial cDNA, full-length cDNA and genomic
genes (chromosomes)

ORF = Open Reading Frame, a defined sequence of amino
acids which can be derived from the cDNA sequence

Contig = A set of DNA sequences that can be combined as a
result of very great similarities into one
sequence (consensus)

Singleton = A contig that contains only one sequence

Module = Domain of a protein with a defined sequence, which
represents one structural unit and which occurs in
various proteins

N = selectively the nucleotide A, T, G or C

X = selectively one of the 20 naturally occurring
amino acids

Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area
maximum pads per read = maximum number of insertions
maximum percent mismatch = maximum deviation in %

Explanation of Figures

Figure 1 shows the systematic gene search in the
Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

Example 1

Search for Tumor-related Candidate Genes

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the bladder tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another.)

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

Example 2Algorithm for Identification and Lengthening of Partial cDNA Sequences with Altered Expression Pattern

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

2.1 Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) *J. Mol. Biol.* 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) *Nucleic Acids Research* 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) *Proc. Natl. Acad. Sci. USA* 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence *S*, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence *S* which were determined in this way are called electronic Northern Blots.

2.1.1

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 1 was found, which occurs 12.2 x more strongly in the normal bladder tissue than in tumor tissue.

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The result is as follows:

Electronic Northern for SEQ. ID NO.: 1

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0026	12.203	0.0819
Breast	0.0064	0.0056	1.1342	0.8917
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0060	0.0156	0.3838	2.5058
Endocrine tissue	0.0068	0.0201	0.3396	2.9444
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0111	0.0226	0.4909	2.0372
Hematopoietic	0.0107	0.0379	0.2823	3.5422
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0173	0.0234	0.7380	1.3551
Lung	0.0083	0.0184	0.4516	2.2144
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0081	0.0274	0.2974	3.3626
Pancreas	0.0083	0.0110	0.7479	1.3371
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0044	0.0106	0.4095	2.4423
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0132	0.0204	0.7482	1.3366
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0096	0.0000	0.0000	0.0000
Prostate hyperplasia	0.0000	0.0000	0.0000	0.0000
Seminal vesicle	0.0000	0.0000	0.0000	0.0000
Sensory organs	0.0139	0.0000	0.0000	0.0000
White blood cells	0.0000	0.0000	0.0000	0.0000
Cervix	0.0000	0.0000	0.0000	0.0000

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0083
Brain	0.0053
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0253
Suprarenal gland	0.0507
Kidney	0.0000
Placenta	0.0182
Prostate	0.0000
Sensory organs	0.0377
Breast	0.0000
Ovary_n	0.0051
Ovary_t	0.0000
Endocrine tissue	0.0035
Fetal	0.0122
Gastrointestinal	0.0171
Hematopoietic	0.0065
Skin-muscle	0.0077
Testicles	0.0082
Lung	0.0090
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0042
Uterus_n	0.0000

In an analogous procedure, the following Northerns were also found:

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0741	0.0102	7.2459	0.1380
Breast	0.0102	0.0038	2.7221	0.3574
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0046	0.8283	1.2072
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0061	0.8467	1.1810
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0017	0.0055	0.2991	3.3428
Penis	0.0102	0.0267	0.4493	2.2259
Prostate	0.0109	0.0064	1.7060	0.5862
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0052			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

Electronic Northern for SEQ. ID NO.: 3

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
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Bladder	0.0595	0.0153	3.8136	0.2622
Breast	0.0064	0.0000	undef	0.0000
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0204	0.0100	2.0377	0.4907
Gastrointestinal	0.0077	0.0046	1.6567	0.6036
Brain	0.0059	0.0092	0.6400	1.5626
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0104	0.0020	5.0803	0.1958
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0217	0.0068	3.1722	0.3152
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0654	0.0362	1.8064	0.5536
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0204	0.3741	2.6732
Uterus-general	0.0000	0.1908	0.0000	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0803			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS % frequency

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0128
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0162
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0164
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0333

Electronic Northern for SEQ. ID NO.: 4

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0351	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 6

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0390	0.0026	15.2544	0.0656
Breast	0.0460	0.0056	8.1663	0.1225
Small intestine	0.0123	0.0331	0.3707	2.6973
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0119	0.0050	2.3774	0.4206
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0052	0.0072	0.7200	1.3890
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0294	0.0000	undef	0.0000
Hepatic	0.0143	0.0065	2.2059	0.4533
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0103	0.0240	0.4283	2.3347
Kidney	0.0516	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.1087			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0319			
Cervix				

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0557
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0498
Lung	0.0036
Suprenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0251

Breast	0.0272
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0116
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles	0.0000
Lung	0.0000
Nerves	0.0151
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0208

Electronic Northern for SEQ. ID NO.: 7

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0351	0.0025	13.7290	0.0728
Breast	0.0051	0.0038	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0060	0.0000	undef	0.0000
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0057	0.0046	1.2425	0.8049
Brain	0.0044	0.0000	undef	0.0000
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0021	0.0137	0.1542	6.4853
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000	0.0032	0.0000	0.0000
Prostate hyperplasia	0.0000	0.0000	0.0000	0.0000
Seminal vesicle	0.0000	0.0000	0.0000	0.0000
Sensory organs	0.0035	0.0000	0.0000	0.0000
White blood cells	0.0000	0.0000	0.0000	0.0000
Cervix				

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

FETUS % frequency	Breast	0.0000
	Ovary_n	0.0000
	Ovary_t	0.0000
	Endocrine tissue	0.0047
	Fetal	0.0000
	Gastrointestinal	0.0000
	Hematopoietic	0.0065
	Skin-muscle	0.0000
	Testicles	0.0000
	Lung	0.0040
	Nerves	0.0000
	Prostate	0.0000
	Sensory Organs	0.0042
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 8

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0051	0.4320	2.3149
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0041	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0055	0.2991	3.3428
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0043	1.5354	0.6513
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			
Cervix	0.0000			

FETUS % frequency

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Development	0.0139	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 9

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0273	0.0026	10.6781	0.0936
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0060	0.0052	1.1513	0.8586
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0046	0.8283	1.2072
Brain	0.0037	0.0051	0.7200	1.3890
Hematopoietic	0.0000	0.0379	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0042	0.0020	2.0321	0.4921
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0060	0.8567	1.1673
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0000	0.0085	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0052			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0490
Skin	Fetal	0.0017
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0114
Lung	Skin-muscle	0.0194
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0040
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 12

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0858	0.0358	2.3971	0.4172
Breast	0.0435	0.0338	1.2854	0.7779
Small intestine	0.0276	0.0165	1.6683	0.5994
Ovary	0.0120	0.0182	0.6579	1.5201
Endocrine tissue	0.0290	0.0176	1.6496	0.6062
Gastrointestinal	0.0594	0.0231	2.5679	0.3894
Brain	0.0333	0.0657	0.5062	1.9754
Hematopoietic	0.0134	0.0000	undef	0.0000
Skin	0.0514	0.0000	undef	0.0000
Hepatic	0.0381	0.0129	2.9412	0.3400
Heart	0.0413	0.0275	1.5034	0.6652
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0384	0.0164	2.3497	0.4256
Stomach-esophagus	0.0290	0.0307	0.9454	1.0578
Muscle-skeleton	0.0188	0.0360	0.5235	1.9102
Kidney	0.0217	0.0548	0.3965	2.5219
Pancreas	0.0132	0.0166	0.7977	1.2536
Penis	0.0779	0.0000	undef	0.0000
Prostate	0.0632	0.0447	1.4136	0.7074
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0068	3.3668	0.2970
Uterus-general	0.0306	0.0000	undef	0.0000
Breast hyperplasia	0.0416			
Prostate hyperplasia	0.0595			
Seminal vesicle	0.0712			
Sensory organs	0.0119			
White blood cells	0.0087			
Cervix	0.0426			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.1293
Gastrointestinal	0.0250	Ovary_n	0.1595
Brain	0.0063	Ovary_t	0.0101
Hematopoietic	0.0118	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0338
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0162
Suprarenal gland	0.0104	Testicles	0.0000
Kidney	0.0185	Lung	0.0410
Placenta	0.0242	Nerves	0.00301
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0628	Sensory Organs	0.0624
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 13

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0468	0.0077	6.1018	0.1639
Breast	0.0294	0.0075	3.9130	0.2556
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0090	0.0000	undef	0.0000
Endocrine tissue	0.0085	0.0050	1.6981	0.5889
Gastrointestinal	0.0192	0.0000	undef	0.0000
Brain	0.0059	0.0062	0.9599	1.0417
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0808	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0540	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0156	0.0082	1.9051	0.5249
Stomach-esophagus	0.0193	0.0077	2.5211	0.3967
Muscle-skeleton	0.1216	0.0000	undef	0.0000
Kidney	0.0000	0.0274	0.0000	undef
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.1587	0.0000	undef	0.0000
Prostate	0.0087	0.0106	0.8189	1.2211
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0457	0.0272	1.6834	0.5940
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0426			

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

FETUS % frequency	Breast	0.0000
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0029
Skin	Fetal	0.0244
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0032
Lung	Skin-muscle	0.0309
Suprarenal gland	Testicles	0.0082
Kidney	Lung	0.0090
Placenta	Nerves	0.0000
Prostate	Prostate	0.0077
Sensory organs	Sensory Organs	0.0208
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 14

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0351	0.0026	13.7290	0.0728
Breast	0.0102	0.0075	1.3611	0.7347
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0090	0.0026	3.4538	0.2895
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0115	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0233	0.0137	1.6961	0.5896
Testicles	0.0000	0.0000	undef	undef
Lung	0.0135	0.0041	3.3022	0.3028
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0634	0.0000	undef	0.0000
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0359	0.0000	undef	0.0000
Prostate	3.0218	0.0043	5.1181	0.1954
Uterus-endometrium	3.0213	0.0000	undef	0.0000
Uterus-myometrium	3.0229	0.0000	undef	0.0000
Uterus-general	3.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0507	Testicles	0.0000
Kidney	0.0062	Lung	0.0181
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0583
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 17

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0273	0.0026	10.6781	0.0936
Breast	0.0307	0.0038	8.1663	0.1225
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0249	0.0000	undef	0.0000
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0367	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0062	0.0020	3.0482	0.3281
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0274	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0120	0.0267	0.4493	2.2259
Penis	0.0087	0.0000	undef	0.0000
Prostate	0.0135	0.0000	undef	0.0000
Uterus-endometrium	0.0229	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0288			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

FETUS % frequency	Breast	0.0204
Development	Ovary_n	0.0000
Gastrointestinal	Ovary_t	0.0051
Brain	Endocrine tissue	0.0000
Hematopoietic	Fetal	0.0047
Skin	Gastrointestinal	0.0000
Hepatic	Hematopoietic	0.0000
Heart-blood vessels	Skin-muscle	0.0000
Lung	Testicles	0.0000
Suprarenal gland	Lung	0.0000
Kidney	Nerves	0.0000
Placenta	Prostate	0.0000
Prostate	Sensory Organs	0.0083
Sensory organs	Uterus_n	

Electronic Northern for SEQ. ID NO.: 18

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0585	0.0230	2.5424	0.3933
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0368	0.0165	2.2244	0.4496
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0115	0.0046	2.4850	0.4024
Brain	0.0022	0.0031	0.7200	1.3890
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0000	0.0020	0.0000	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0509	0.0000	undef	0.0000
Prostate	0.0218	0.0149	1.4623	0.6838
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0543	0.4208	2.3761
Uterus-general	0.0407	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0356			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0108
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000
Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0030
Nerves	0.0137
Prostate	0.0000
Sensory Organs	0.0083
Uterus_n	

Electronic Northern for SEQ. ID NO.: 20

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0429	0.0153	2.7966	0.3576
Breast	0.0141	0.0282	0.4991	2.0038
Small intestine	0.0307	0.0165	1.8537	0.5395
Ovary	0.0300	0.0390	0.7675	1.3029
Endocrine tissue	0.0409	0.0176	2.3288	0.4294
Gastrointestinal	0.0230	0.0139	1.6567	0.6036
Brain	0.0200	0.0298	0.6703	1.4919
Hematopoietic	0.0160	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0143	0.0259	0.5515	1.8133
Heart	0.0339	0.0000	undef	0.0000
Testicles	0.0288	0.0234	1.2299	0.8130
Lung	0.0270	0.0409	0.6604	1.5141
Stomach-esophagus	0.0483	0.0230	2.1009	0.4760
Muscle-skeleton	0.0394	0.0240	1.6419	0.6090
Kidney	0.0244	0.0205	1.1896	0.8406
Pancreas	0.0198	0.0276	0.7180	1.3928
Penis	0.0359	0.0533	0.6739	1.4839
Prostate	0.0305	0.0255	1.1942	0.8374
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0534	0.0272	1.9640	0.5092
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0595			
Prostate hyperplasia	0.0267			
Seminal vesicle	0.0118			
Sensory organs	0.0286			
White blood cells	0.0426			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	
Gastrointestinal	0.0000
Brain	0.0222
Hematopoietic	0.0063
Skin	0.0079
Hepatic	0.0000
Heart-blood vessels	0.0285
Lung	0.0470
Suprarenal gland	0.0000
Kidney	0.0247
Placenta	0.0121
Prostate	0.0249
Sensory organs	0.0377
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0082
Nerves	0.0080
Prostate	0.0205
Sensory Organs	0.0000
Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 21

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
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Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0034	0.0150	0.2264	4.4166
Gastrointestinal	0.0000	0.0139	0.0000	undef
Brain	0.0177	0.0031	5.7597	0.1736
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0031	0.0123	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0135	0.0000	undef	0.0000
Uterus-endometrium	0.0076	0.0068	1.1223	0.6911
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS % frequency

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0142	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0070
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 22

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0152	0.0068	2.2445	0.4453
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0023
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 23

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0390	0.0000	undef	0.0000
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0115	0.0046	2.4850	0.4024
Brain	0.0022	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0240	0.0000	undef	0.0000
Prostate	0.0065	0.0064	1.0236	0.9769
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0475	0.4810	2.0791
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0149			
Prostate hyperplasia	0.0267			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

TOPBEDS - PREPARED

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0249
Sensory organs	0.0000
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0006
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 24

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0351	0.0051	6.8645	0.1457
Breast	0.0026	0.0056	0.4537	2.2042
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0090	0.0130	0.6908	1.4477
Endocrine tissue	0.0068	0.0075	0.9057	1.1042
Gastrointestinal	0.0172	0.0139	1.2425	0.8048
Brain	0.0044	0.0082	0.5400	1.8520
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0042	0.0143	0.2903	3.4446
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0000	0.0205	0.0000	undef
Pancreas	0.0033	0.0110	0.2991	3.3428
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0087	0.0128	0.6824	1.4654
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0035			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0181
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0130
Suprarenal gland	0.0254	Testicles	0.0154
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0060
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0416

Electronic Northern for SEQ. ID NO.: 25

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	
Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 26

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0429	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0043	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0235			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0245
Hematopoietic	0.0000	Endocrine tissue	0.0012
Skin	0.0000	Fetal	0.0000
Hepatic	0.0260	Gastrointestinal	0.0171
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 27

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0312	0.0000	undef	0.0000
Breast	0.0090	0.0055	1.5879	0.6298
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0052	1.1513	0.8686
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0030	0.0051	0.5760	1.7362
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0021	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0065	0.0043	1.5334	0.6513
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0059	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0009	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0245
Hematopoietic	Endocrine tissue	0.0064
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0114
Heart-blood vessels	Hematopoietic	0.0065
Lung	Skin-muscle	0.0154
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0050
Placenta	Nerves	0.0205
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0167
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 29

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0312	0.0051	6.1018	0.1639
Breast	0.0307	0.0019	16.3327	0.0612
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0120	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0075	0.0000	undef
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0015	0.0062	0.2400	4.1669
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0138	0.0412	0.3341	2.9932
Testicles	0.0403	0.0000	undef	0.0000
Lung	0.0114	0.0061	1.8628	0.5368
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0274	0.0300	0.9138	1.0944
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0050	0.0331	0.1496	6.6857
Penis	0.0359	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0686	0.0679	1.0100	0.9901
Uterus-general	0.0458	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0213			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0051
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0023
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0097
Suprarenal gland	Testicles	0.0077
Kidney	Lung	0.0010
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0250
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 30

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder	0.0273	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	0.0000
Lung	0.0021	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0021	1.0236	0.9789
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

	FETUS	
	% frequency	STANDARDIZED/SUBTRACTED
Development	0.0000	LIBRARIES
Gastrointestinal	0.0056	% frequency
Brain	0.0000	
Hematopoietic	0.0000	
Skin	0.0000	
Hepatic	0.0000	
Heart-blood vessels	0.0000	
Lung	0.0000	
Suprarenal gland	0.0000	
Kidney	0.0000	
Placenta	0.0000	
Prostate	0.0000	
Sensory organs	0.0000	

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0010
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0125
Uterus_n	

Electronic Northern for SEQ. ID NO.: 31

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0038	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	0.0000
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0080	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0499	Prostate	0.0000
Sensory organs	0.0000	Sensory_Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 32

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0234	0.0026	9.1527	0.1093
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0038	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0121	Nerves	0.0068
Prostate	0.0000	Prostate	0.0077
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 33

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0104	0.5756	1.7372
Endocrine tissue	0.0085	0.0150	0.5660	1.7667
Gastrointestinal	0.0019	0.0139	0.1381	7.2434
Brain	0.0037	0.0010	3.5998	0.2778
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0042	0.0061	0.6774	1.4763
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0109	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0076	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0023
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0130
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0082
Kidney	Lung	0.0070
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0042
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 34

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 35

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0050	0.2856	3.5020
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0310
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 36

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 37

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
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Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0090	0.0052	1.7269	0.5791
Endocrine tissue	0.0068	0.0025	2.7170	0.3681
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0089	0.0144	0.6171	1.6205
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0135	0.0123	1.1007	0.9085
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0034	0.0120	0.2856	3.5020
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0022	0.0149	0.1462	6.8384
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0255	0.1908	0.1334	7.4943
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0104			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.1595
Brain	Ovary_t	0.0253
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0116
Hepatic	Gastrointestinal	0.0366
Heart-blood vessels	Hematopoietic	0.0456
Lung	Skin-muscle	0.0162
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0221
Placenta	Nerves	0.0068
Prostate	Prostate	0.0077
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 38

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0273	0.0051	5.3391	0.1873
Breast	0.0026	0.0075	0.3403	2.9389
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0068	0.0125	0.5434	1.8403
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0081	0.0031	2.6399	0.3788
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0102	0.4064	2.4605
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0136	0.0205	0.6609	1.5132
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0109	0.0021	5.1181	0.1954
Uterus-endometrium	0.0068	0.0528	0.1280	7.8106
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0128	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0089	undef	undef
Seminal vesicle	0.0235	0.0009	undef	undef
Sensory organs	0.0009	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0051
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0012
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0164
Placenta	Nerves	0.0070
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 39

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 40

	NORMAL % frequency	TUMOR % frequency	RatioS N/T	T/N
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Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0007	0.0031	0.2400	4.1669
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0058	0.0000	undef	0.0000
Testicles	0.0021	0.0041	0.5080	1.9684
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0086	0.0000	undef	0.0000
Muscle-skeleton	0.0027	0.0000	undef	0.0000
Kidney	0.0033	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0227
Suprarenal gland	0.0254	Testicles	0.0077
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 43

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0030	0.0000	undef	0.0000
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0041	1.2701	0.7873
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0055	0.2391	3.3428
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0118	0.0000	undef	undef
Sensory organs	0.0017	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
----------------------	---

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 44

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 46

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 47

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0273	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory_Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 48

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0273	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0049	0.0000	undef	0.0000
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0010	0.0020	0.5080	1.9684
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0034	0.0000	undef	0.0000
Muscle-skeleton	0.0027	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0021	1.0236	0.9769
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

FETUS			
% frequency			
Development	0.0278	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0017
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0060
Placenta	0.0061	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 50

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix				

FETUS
% frequency

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 51		NORMAL		TUMOR		Ratios	
		% frequency	% frequency	N/T	T/N		
Bladder	0.0156	0.0000	0.0000	undef	0.0000		
Breast	0.0026	0.0000	0.0000	undef	0.0000		
Small intestine	0.0000	0.0000	0.0000	undef	undef		
Ovary	0.0060	0.0078	0.0078	0.7675	1.3029		
Endocrine tissue	0.0034	0.0025	0.0000	1.3585	0.7361		
Gastrointestinal	0.0057	0.0000	0.0000	undef	0.0000		
Brain	0.0022	0.0021	0.0000	1.0799	0.9260		
Hematopoietic	0.0027	0.0000	0.0000	undef	0.0000		
Skin	0.0000	0.0000	0.0000	undef	undef		
Hepatic	0.0000	0.0000	0.0000	undef	undef		
Heart	0.0053	0.0000	0.0000	undef	0.0000		
Testicles	0.0000	0.0000	0.0000	undef	undef		
Lung	0.0031	0.0000	0.0000	undef	undef		
Stomach-esophagus	0.0000	0.0000	0.0000	undef	undef		
Muscle-skeleton	0.0000	0.0000	0.0000	undef	undef		
Kidney	0.0000	0.0000	0.0166	0.0000	undef		
Pancreas	0.0000	0.0000	0.0000	undef	undef		
Penis	0.0022	0.0000	0.0000	undef	0.0000		
Prostate	0.0068	0.0000	0.0000	undef	0.0000		
Uterus-endometrium	0.0000	0.0000	0.0000	undef	undef		
Uterus-myometrium	0.0000	0.0000	0.0000	undef	undef		
Uterus-general	0.0032	0.0000	0.0000	undef	undef		
Breast hyperplasia	0.0059	0.0000	0.0000	undef	undef		
Prostate hyperplasia	0.0000	0.0000	0.0000	undef	undef		
Seminal vesicle	0.0000	0.0000	0.0000	undef	undef		
Sensory organs	0.0026	0.0000	0.0000	undef	undef		
White blood cells	0.0000	0.0000	0.0000	undef	undef		
Cervix							

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

Electronic Northern for SEQ. ID NO.: 52

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0312	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix				

PROTECTED - DRAFT RELEASED

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 53

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	0.0000
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0027	0.0000	undef	0.0000
Kidney	0.0000	0.0055	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0076	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0032
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory_Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 54

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0020	0.0000	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0055	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0076	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0057
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory_Organs	0.0000
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 55

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 56

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0093	0.4142	2.4145
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0030	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0009	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0228
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0000	Lung	0.0040
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 57

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0065	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0058	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 58

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0026	9.1527	0.1093
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 59

	NORMAL % frequency	TUMOR % frequency	Ratios		
			N/T	T/N	
Bladder	0.0273	0.0000	undef	0.0000	
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0117	0.0000	undef	
Testicles	0.0000	0.0020	0.0000	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.0000	undef	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000				
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency		
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 60

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0051	0.0038	1.3611	0.7347
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0022	0.0021	1.0799	0.9260
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032	0.0000	undef	0.0000
Prostate hyperplasia	0.0000	0.0000	undef	0.0000
Seminal vesicle	0.0000	0.0000	undef	0.0000
Sensory organs	0.0099	0.0000	undef	0.0000
White blood cells	0.0000	0.0000	undef	0.0000
Cervix	0.0000	0.0000	undef	0.0000

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency		
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0070
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 61

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0067	0.0051	1.2959	0.7716
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	0.0000
Heart	0.0074	0.0000	0.0000	undef
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0031	0.0061	0.5080	1.9684
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0034	0.0120	0.2856	3.5020
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0066	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0000	0.0030		
Prostate hyperplasia	0.0000	0.0000		
Seminal vesicle	0.0000	0.0000		
Sensory organs	0.0061	0.0000		
White blood cells	0.0000	0.0000		
Cervix				

STANDARDIZED/SUBTRACTED

FETUS % frequency	LIBRARIES % frequency		
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0010
Prostate	0.0249	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 62

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0043	0.0000	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0068
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0063
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0006
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 63

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0351	0.0051	6.8645	0.1457
Breast	0.0026	0.0075	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0015	0.0041	0.3600	2.7779
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0042	0.0041	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0120	0.0000	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0009			
White blood cells	0.0106			
Cervix				

TRANSLATED

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0012
Skin	Fetal	0.0122
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0097
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0050
Placenta	Nerves	0.0068
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0042
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 65

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED LIBRARIES	
% frequency	% frequency	

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0077
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 67

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
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Bladder	0.0390	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0235	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0057
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 69

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0858	0.0077	11.1866	0.0894
Breast	0.0102	0.0075	1.3611	0.7347
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0060	0.0260	0.2303	4.3431
Endocrine tissue	0.0068	0.0125	0.5434	1.8403
Gastrointestinal	0.0038	0.0278	0.1381	7.2434
Brain	0.0022	0.0144	0.1543	6.4818
Hematopoietic	0.0013	0.0379	0.0353	28.3379
Skin	0.0734	0.1695	0.4332	2.3084
Hepatic	0.0000	0.0194	0.0000	undef
Heart	0.0159	0.0137	1.1565	0.8647
Testicles	0.0000	0.0468	0.0000	undef
Lung	0.0073	0.0164	0.4445	2.2496
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0069	0.0180	0.3807	2.6265
Kidney	0.0163	0.0000	undef	0.0000
Pancreas	0.0066	0.0055	1.1966	0.8357
Penis	0.0210	0.0267	0.7862	1.2719
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0000			
Cervix				

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

FETUS % frequency	Breast	0.0000
Development	Ovary_n	0.0051
Gastrointestinal	Ovary_t	0.0245
Brain	Endocrine tissue	0.0128
Hematopoietic	Fetal	0.0000
Skin	Gastrointestinal	0.0000
Hepatic	Hematopoietic	0.0227
Heart-blood vessels	Skin-muscle	0.0154
Lung	Testicles	0.0000
Suprarenal gland	Lung	0.0171
Kidney	Nerves	0.0068
Placenta	Prostate	0.0155
Prostate	Sensory Organs	0.0000
Sensory organs	Uterus_n	

Electronic Northern for SEQ. ID NO.: 72

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0585	0.0077	7.6272	0.1311
Breast	0.0192	0.0019	10.2079	0.0980
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0090	0.0052	1.7269	0.5791
Endocrine tissue	0.0000	0.0075	0.0000	undef
Gastrointestinal	0.0307	0.0000	undef	0.0000
Brain	0.0118	0.0062	1.9199	0.5209
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0190	0.0055	2.9412	0.3400
Heart	0.0244	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0085	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0509	0.0000	undef	0.0000
Prostate	0.0153	0.0085	1.7913	0.5562
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0320			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0204	
Gastrointestinal	0.0000	Breast
Brain	0.0167	Ovary_n
Hematopoietic	0.0000	Ovary_t
Skin	0.0000	Endocrine tissue
Hepatic	0.0000	Fetal
Heart-blood vessels	0.0071	Gastrointestinal
Lung	0.0036	Hematopoietic
Suprarenal gland	0.0000	Skin-muscle
Kidney	0.0000	Testicles
Placenta	0.0061	Lung
Prostate	0.0000	Nerves
Sensory organs	0.0251	Prostate
		Sensory Organs
		Uterus_n

Electronic Northern for SEQ. ID NO.: 73

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	
Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory_Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 75

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS % frequency	
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES

% frequency	
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory_Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 77

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
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Bladder	0.0351	0.0051	6.8645	0.1457
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0104	0.0000	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0067	0.0010	6.4796	0.1543
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0117	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0137	0.3965	2.5219
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0229	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0087
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0057
Lung	Skin-muscle	0.0130
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0090
Placenta	Nerves	0.0068
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0458
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 78		NORMAL		TUMOR		Ratios	
		% frequency		% frequency		N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000			
Breast	0.0000	0.0000	undef	undef			
Small intestine	0.0000	0.0000	undef	undef			
Ovary	0.0000	0.0000	undef	undef			
Endocrine tissue	0.0000	0.0000	undef	undef			
Gastrointestinal	0.0000	0.0093	0.0000	undef			
Brain	0.0000	0.0000	undef	undef			
Hematopoietic	0.0013	0.0000	undef	0.0000			
Skin	0.0000	0.0000	undef	undef			
Hepatic	0.0000	0.0000	undef	undef			
Heart	0.0011	0.0412	0.0257	38.9118			
Testicles	0.0000	0.0000	undef	undef			
Lung	0.0000	0.0020	0.0000	undef			
Stomach-esophagus	0.0000	0.0000	undef	undef			
Muscle-skeleton	0.0000	0.0000	undef	undef			
Kidney	0.0000	0.0000	undef	undef			
Pancreas	0.0000	0.0000	undef	undef			
Penis	0.0000	0.0000	undef	undef			
Prostate	0.0000	0.0000	undef	undef			
Uterus-endometrium	0.0000	0.0000	undef	undef			
Uterus-myometrium	0.0000	0.0000	undef	undef			
Uterus-general	0.0000						
Breast hyperplasia	0.0000						
Prostate hyperplasia	0.0000						
Seminal vesicle	0.0000						
Sensory organs	0.0000						
White blood cells	0.0000						
Cervix							
STANDARDIZED/SUBTRACTED							
FETUS		LIBRARIES					
% frequency		% frequency					
Development	0.0278	Breast	0.0000				
Gastrointestinal	0.0000	Ovary_n	0.0000				
Brain	0.0000	Ovary_t	0.0000				
Hematopoietic	0.0000	Endocrine tissue	0.0000				
Skin	0.0000	Fetal	0.0000				
Hepatic	0.0000	Gastrointestinal	0.0000				
Heart-blood vessels	0.0000	Hematopoietic	0.0000				
Lung	0.0000	Skin-muscle	0.0000				
Suprarenal gland	0.0000	Testicles	0.0000				
Kidney	0.0000	Lung	0.0000				
Placenta	0.0000	Nerves	0.0000				
Prostate	0.0000	Prostate	0.0000				
Sensory organs	0.0000	Sensory Organs	0.0000				
		Uterus_n	0.0000				

Electronic Northern for SEQ. ID NO.: 79

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0351	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 80

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0624	0.0102	6.1018	0.1639
Breast	0.0141	0.0056	2.4953	0.4008
Small intestine	0.0215	0.0000	undef	0.0000
Ovary	0.0150	0.0078	1.9188	0.5212
Endocrine tissue	0.0187	0.0050	3.7359	0.2677
Gastrointestinal	0.0307	0.0139	2.2089	0.4527
Brain	0.0214	0.0082	2.6099	0.3832
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0190	0.0065	2.9412	0.3400
Heart	0.0360	0.0137	2.6213	0.3815
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0041	2.0321	0.4921
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0171	0.0060	2.8555	0.3502
Kidney	0.0136	0.0548	0.2478	4.0351
Pancreas	0.0083	0.0387	0.2137	4.6800
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0087	0.0064	1.3648	0.7327
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0288			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.1246			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0000			

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 82

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0390	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 83

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
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Bladder	0.0273	0.0026	10.6781	0.0936
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0229	0.0031	7.4396	0.1344
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0253
Hematopoietic	0.0000	Endocrine tissue	0.0006
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0201
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0310
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 85

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix	0.0000	0.0000	undef	undef

PROTECTED - UNCLASSIFIED

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	0.0000
Gastrointestinal	0.0000	0.0000
Brain	0.0000	0.0000
Hematopoietic	0.0000	0.0000
Skin	0.0000	0.0000
Hepatic	0.0000	0.0000
Heart-blood vessels	0.0000	0.0000
Lung	0.0000	0.0000
Suprarenal gland	0.0000	0.0000
Kidney	0.0000	0.0000
Placenta	0.0000	0.0000
Prostate	0.0000	0.0000
Sensory organs	0.0000	0.0000
	Breast	0.0000
	Ovary_n	0.0000
	Ovary_t	0.0000
	Endocrine tissue	0.0000
	Fetal	0.0000
	Gastrointestinal	0.0000
	Hematopoietic	0.0000
	Skin-muscle	0.0000
	Testicles	0.0000
	Lung	0.0000
	Nerves	0.0000
	Prostate	0.0000
	Sensory Organs	0.0000
	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 86

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
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Bladder	0.0273	0.0051	5.3391	0.1873
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0041	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 88

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000
Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0386
Testicles	0.0000
Lung	0.0000
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0208
Uterus_n	

Electronic Northern for SEQ. ID NO.: 90

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0312	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0006
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0010
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 92

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0051	6.1018	0.1639
Breast	0.0102	0.0113	0.9074	1.1021
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0051	0.0125	0.4075	2.4537
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0067	0.0329	0.2025	4.9386
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0330	0.0000	undef	0.0000
Hepatic	0.0333	0.0323	1.0294	0.9714
Heart	0.0127	0.0137	0.9252	1.0809
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0156	0.0082	1.9051	0.5249
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0120	0.4283	2.3347
Kidney	0.0027	0.0205	0.1322	7.5658
Pancreas	0.0050	0.0110	0.4487	2.2286
Penis	0.0060	0.0267	0.2246	4.4517
Prostate	0.0131	0.0128	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0147			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0072
Suprarenal gland	0.0000
Kidney	0.0545
Placenta	0.0000
Prostate	0.0000
Sensory organs	
	Breast
	Ovary_n
	Ovary_t
	Endocrine tissue
	Fetal
	Gastrointestinal
	Hematopoietic
	Skin-muscle
	Testicles
	Lung
	Nerves
	Prostate
	Sensory Organs
	Uterus_n

Electronic Northern for SEQ. ID NO.: 93

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0166	0.0226	0.7372	1.3584
Small intestine	0.0000	0.0155	0.0000	undef
Ovary	0.0270	0.0000	undef	0.0000
Endocrine tissue	0.0238	0.0276	0.8645	1.1567
Gastrointestinal	0.0115	0.0093	1.2425	0.8048
Brain	0.0089	0.0072	1.2342	0.8102
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0143	0.0518	0.2757	3.6266
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0230	0.0117	1.9679	0.5082
Lung	0.0218	0.0266	0.8207	1.2185
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0081	0.0137	0.5948	1.6813
Pancreas	0.0149	0.0221	0.6731	1.4857
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0240	0.0213	1.1260	0.8881
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0340	0.6734	1.4851
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0224			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0445			
Sensory organs	0.0235			
White blood cells	0.0009			
Cervix	0.0213			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0099
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0065
Lung	Skin-muscle	0.0154
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0020
Placenta	Nerves	0.0068
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0042
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 94

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0195	0.0026	7.6272	0.1311
Breast	0.0051	0.0094	0.5444	1.8368
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0119	0.0150	0.7925	1.2619
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0030	0.0103	0.2880	3.4724
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0020	2.5402	0.3937
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0017	0.0120	0.1428	7.0404
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0381	0.0068	5.6113	0.1782
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0095			
Cervix	0.0106			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0204
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0709
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.2513	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0228
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0185	Lung	0.0010
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0250
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 95

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0351	0.0026	13.7290	0.0728
Breast	0.0026	0.0094	0.2722	3.6736
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0075	0.0000	undef
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0037	0.0051	0.7200	1.3890
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0190	0.0129	1.4706	0.6800
Heart	0.0084	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0021	0.0061	0.3387	2.9526
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0050	0.0166	0.2991	3.3428
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0106	0.4095	2.4423
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0061			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0116
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0194
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0082
Placenta	Nerves	0.0010
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0155
	Uterus_n	0.0208

Electronic Northern for SEQ. ID NO.: 96

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
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Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0090	0.0094	0.9527	1.0496
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0153	0.0176	0.8733	1.1451
Gastrointestinal	0.0096	0.0185	0.5177	1.9316
Brain	0.0081	0.0031	2.6399	0.3788
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0020	2.5402	0.3937
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0130	0.0000	undef	0.0000
Prostate	0.0022	0.0064	0.3412	2.9308
Uterus-endometrium	0.0135	0.0528	0.2561	3.9053
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0139	Breast	0.0000
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0324
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0328
Placenta	0.0061	Nerves	0.0141
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0167
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 97

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0064	0.0038	1.7013	0.5878
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0156	0.1919	5.2117
Endocrine tissue	0.0136	0.0251	0.5434	1.8403
Gastrointestinal	0.0134	0.0139	0.9664	1.0348
Brain	0.0074	0.0277	0.2667	3.7502
Hematopoietic	0.0134	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0127	0.0412	0.3084	3.2426
Testicles	0.0115	0.0585	0.1968	5.0816
Lung	0.0104	0.0204	0.5080	1.9684
Stomach-esophagus	0.0120	0.0240	0.4997	2.0011
Muscle-skeleton	0.0054	0.0068	0.7930	1.2610
Kidney	0.0083	0.0331	0.2493	4.0114
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0240	0.0277	0.8661	1.1545
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0152	0.0000	undef	0.0000
Uterus-myometrium	0.0153	0.0000	undef	0.0000
Uterus-general	0.0064			
Breast hyperplasia	0.0178			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0113			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0181
Suprarenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0249
Sensory organs	0.0000
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0082
Lung	0.0070
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 98

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0026	0.0113	0.2268	4.4083
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0119	0.0100	1.1887	0.8413
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0229	0.0062	3.7198	0.2688
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0847	0.0000	undef
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0062	0.0041	1.5241	0.6561
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0033	0.0055	0.5983	1.5714
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0061			
White blood cells	0.0106			
Cervix				

FETUS % frequency	
Development	0.0557
Gastrointestinal	0.0083
Brain	0.0188
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0000
Suprarenal gland	0.0254
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0243
Fetal	0.0175
Gastrointestinal	0.0000
Hematopoietic	0.0114
Skin-muscle	0.0389
Testicles	0.0164
Lung	0.0251
Nerves	0.0000
Prostate	0.0310
Sensory Organs	0.0208
Uterus_n	

Electronic Northern for SEQ. ID NO.: 99

	NORMAL % frequency	TUMOR % frequency	Ratio N/T	Ratio T/N
Bladder	0.0312	0.0026	12.2035	0.0819
Breast	0.0166	0.0132	1.2638 0.7912	
Small intestine	0.0061	0.0000	undef 0.0000	
Ovary	0.0090	0.0026	3.4538 0.2895	
Endocrine tissue	0.0085	0.0025	3.3962 0.2944	
Gastrointestinal	0.0115	0.0231	0.4970 2.0121	
Brain	0.0074	0.0082	0.8999 1.1112	
Hematopoietic	0.0120	0.0379	0.3176 3.1487	
Skin	0.0147	0.0000	undef 0.0000	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0085	0.0275	0.3084 3.2426	
Testicles	0.0058	0.0000	undef 0.0000	
Lung	0.0104	0.0061	1.6934 0.5905	
Stomach-esophagus	0.0193	0.0000	undef 0.0000	
Muscle-skeleton	0.0051	0.0180	0.2856 3.5020	
Kidney	0.0109	0.0274	0.3965 2.5219	
Pancreas	0.0017	0.0000	undef 0.0000	
Penis	0.0150	0.0000	undef 0.0000	
Prostate	0.0022	0.0000	undef 0.0000	
Uterus-endometrium	0.0203	0.0000	undef 0.0000	
Uterus-myometrium	0.0000	0.0000	undef undef	
Uterus-general	0.0255	0.0000	undef 0.0000	
Breast hyperplasia	0.0224	0.0059		
Prostate hyperplasia	0.0059	0.0089		
Seminal vesicle	0.0018	0.0113		
Sensory organs	0.0113	0.0106		
White blood cells	0.0106			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0051
Hematopoietic	Ovary_t 0.0000
Skin	Endocrine tissue 0.0000
Hepatic	Fetal 0.0035
Heart-blood vessels	Gastrointestinal 0.0000
Lung	Hematopoietic 0.0057
Suprarenal gland	Hematopoietic 0.0130
Kidney	Skin-muscle 0.0000
Placenta	Testicles 0.0000
Prostate	Lung 0.0040
Sensory organs	Nerves 0.0205
	Prostate 0.0000
	Sensory Organs 0.0042
	Uterus_n 0.0042

Electronic Northern for SEQ. ID NO.: 100

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0051	0.0056	0.9074	1.1021
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0000	0.0075	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0030	0.0051	0.5760	1.7362
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0137	0.1542	6.4853
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0041	1.2701	0.7873
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0061			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 101

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0234	0.0026	9.1527 0.1093
Breast	0.0077	0.0094	0.8166 1.2245
Small intestine	0.0123	0.0000	undef 0.0000
Ovary	0.0060	0.0000	undef 0.0000
Endocrine tissue	0.0034	0.0050	0.6792 1.4722
Gastrointestinal	0.0057	0.0139	0.4142 2.4145
Brain	0.0015	0.0021	0.7200 1.3890
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0048	0.0129	0.3676 2.7200
Heart	0.0074	0.0000	undef 0.0000
Testicles	0.0058	0.0000	undef 0.0000
Lung	0.0052	0.0020	2.5402 0.3937
Stomach-esophagus	0.0097	0.0077	1.2605 0.7933
Muscle-skeleton	0.0069	0.0000	undef 0.0000
Kidney	0.0081	0.0137	0.5948 1.6813
Pancreas	0.0000	0.0166	0.0000 undef
Penis	0.0150	0.0800	0.1872 5.3421
Prostate	0.0109	0.0085	1.2795 0.7815
Uterus-endometrium	0.0068	0.0000	undef 0.0000
Uterus-myometrium	0.0076	0.0000	undef 0.0000
Uterus-general	0.0102	0.0000	undef 0.0000
Breast hyperplasia	0.0064		
Prostate hyperplasia	0.0059		
Seminal vesicle	0.0000		
Sensory organs	0.0118		
White blood cells	0.0078		
Cervix	0.0213		

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0408
Gastrointestinal	0.0056	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 102

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Testicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Development	0.0000	Breast	0.0204
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0260	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0030
Placenta	0.0000	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 103

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 104

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N
Bladder	0.0312	0.0051	6.1018 0.1639
Breast	0.0102	0.0056	1.8147 0.5510
Small intestine	0.0092	0.0000	undef 0.0000
Ovary	0.0180	0.0104	1.7269 0.5791
Endocrine tissue	0.0085	0.0176	0.4852 2.0611
Gastrointestinal	0.0172	0.0046	3.7275 0.2683
Brain	0.0126	0.0123	1.0199 0.9804
Hematopoietic	0.0040	0.0758	0.0529 18.8919
Skin	0.0257	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0138	0.0275	0.5011 1.9955
Testicles	0.0058	0.0000	undef 0.0000
Lung	0.0145	0.0102	1.4225 0.7030
Stomach-esophagus	0.0000	0.0077	0.0000 undef
Muscle-skeleton	0.0205	0.0000	undef 0.0000
Kidney	0.0190	0.0137	1.3878 0.7206
Pancreas	0.0050	0.0110	0.4487 2.2286
Penis	0.0180	0.0000	undef 0.0000
Prostate	0.0087	0.0000	undef 0.0000
Uterus-endometrium	0.0203	0.0000	undef 0.0000
Uterus-myometrium	0.0152	0.0136	1.1223 0.8911
Uterus-general	0.0153	0.0000	undef 0.0000
Breast hyperplasia	0.0096		
Prostate hyperplasia	0.0149		
Seminal vesicle	0.0089		
Sensory organs	0.0353		
White blood cells	0.0043		
Cervix	0.0000		

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

FETUS			
% frequency			
Development	0.0000	Breast	0.0204
Gastrointestinal	0.0056	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0253
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0192
Hepatic	0.0260	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0324
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0185	Lung	0.0000
Placenta	0.1030	Nerves	0.0151
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0077
		Uterus_n	0.0208

Electronic Northern for SEQ. ID NO.: 105

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0115	0.0132	0.8750	1.1429
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0090	0.0052	1.7269	0.5791
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0115	0.0000	undef	0.0000
Brain	0.0030	0.0041	0.7200	1.3890
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0127	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0042	0.0000	undef	0.0000
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0109	0.0085	1.2795	0.7615
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0319			

FETUS % frequency

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0125
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0108
Suprarenal gland	0.0254
Kidney	0.0000
Placenta	0.0121
Prostate	0.0249
Sensory organs	0.0000

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0099
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0259
Testicles	0.0000
Lung	0.0082
Nerves	0.0100
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 106

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder				
Breast	0.0312	0.0077	4.0678	0.2458
Small intestine	0.0192	0.0019	10.2079	0.0980
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0060	0.0390	0.1535	6.5146
Gastrointestinal	0.0058	0.0075	0.9057	1.1042
Brain	0.0057	0.0046	1.2425	0.8048
Hematopoietic	0.0118	0.0164	0.7200	1.3890
Skin	0.0080	0.0379	0.2117	4.7230
Hepatic	0.0184	0.0000	undef	0.0000
Heart	0.0000	0.0129	0.0000	undef
Testicles	0.0191	0.0275	0.6939	1.4412
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0239	0.0102	2.3370	0.4279
Muscle-skeleton	0.0000	0.0307	0.0000	undef
Kidney	0.0051	0.0240	0.2142	4.6693
Pancreas	0.0081	0.0137	0.5948	1.6813
Penis	0.0033	0.0110	0.2991	3.3428
Prostate	0.0120	0.0000	undef	0.0000
Uterus-endometrium	0.0022	0.0021	1.0236	0.9769
Uterus-myometrium	0.0068	0.0000	undef	0.0000
Uterus-general	0.0000	0.0204	0.0000	undef
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0320			
Seminal vesicle	0.0059			
Sensory organs	0.0178			
White blood cells	0.0118			
Cervix	0.0087			
	0.0319			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0203
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0198
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0171
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0082
Placenta	Nerves	0.0161
Prostate	Prostate	0.0137
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0208

Electronic Northern for SEQ. ID NO.: 107

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 108

	NORMAL % frequency	TUMOR. % frequency	Ratios N/T	T/N
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Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0038	0.0056	0.6805	1.4694
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0017	0.0100	0.1698	5.8889
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0022	0.0103	0.2160	4.6299
Hematopoietic	0.0027	0.0758	0.0353	28.3379
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0125	0.0061	2.0321	0.4921
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0137	0.0000	undef
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0095			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0759
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0000
Testicles	0.0164
Lung	0.0000
Nerves	0.0274
Prostate	0.0000
Sensory Organs	0.0083
Uterus_n	

Electronic Northern for SEQ. ID NO.: 109

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
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Bladder	0.0507	0.0179	2.8330	0.3530
Breast	0.0153	0.0000	undef	0.0000
Small intestine	0.0276	0.0000	undef	0.0000
Ovary	0.0270	0.0000	undef	0.0000
Endocrine tissue	0.0119	0.0075	1.5849	0.6309
Gastrointestinal	0.0096	0.0046	2.0708	0.4829
Brain	0.0044	0.0010	4.3198	0.2315
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0201	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0073	0.0000	undef	0.0000
Stomach-esophagus	0.0580	0.0230	2.5211	0.3967
Muscle-skeleton	0.0771	0.0000	undef	0.0000
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0033	0.0221	0.1496	6.6857
Penis	0.0210	0.0000	undef	0.0000
Prostate	0.0174	0.0106	1.6378	0.6106
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0068	3.3668	0.2970
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0534			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0816
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0507	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0242	Nerves	0.0030
Prostate	0.0749	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 110

	NORMAL	TUMOR	Ratios
	% frequency	% frequency	N/T T/N

Bladder	0.0156	0.0000	undef 0.0000
Breast	0.0230	0.0038	6.1248 0.1633
Small intestine	0.0031	0.0000	undef 0.0000
Ovary	0.0120	0.0000	undef 0.0000
Endocrine tissue	0.0136	0.0025	5.4340 0.1840
Gastrointestinal	0.0000	0.0000	undef undef
Brain	0.0022	0.0031	0.7200 1.3890
Hematopoietic	0.0027	0.0000	undef 0.0000
Skin	0.0194	0.0000	undef 0.0000
Hepatic	0.0000	0.0065	0.0000 undef
Heart	0.0212	0.0137	1.5420 0.6485
Testicles	0.0000	0.0000	undef undef
Lung	0.0156	0.0164	0.9526 1.0498
Stomach-esophagus	0.0000	0.0077	0.0000 undef
Muscle-skeleton	0.0069	0.0180	0.3807 2.6265
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0017	0.0000	undef 0.0000
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0000	0.0043	0.0000 undef
Uterus-endometrium	0.0068	0.0000	undef 0.0000
Uterus-myometrium	0.0305	0.0068	4.4891 0.2228
Uterus-general	0.0000	0.0000	undef undef
Breast hyperplasia	0.0192	0.0089	
Prostate hyperplasia	0.0089	0.0000	
Seminal vesicle	0.0235	0.0235	
Sensory organs	0.0000	0.0000	
White blood cells	0.0532	0.0532	
Cervix			

FETUS	STANDARDIZED/SUBTRACTED LIBRARIES		
% frequency	% frequency		
Development	0.0417	Breast	0.0204
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0213	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0162
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0000
Placenta	0.0121	Nerves	0.0080
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 111

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0312	0.0026	12.2035	0.0819
Breast	0.0051	0.0019	2.7221	0.3674
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0022	0.0041	0.5400	1.8520
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0011	0.0137	0.0771	12.9706
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0017	0.0055	0.2991	3.3428
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0019
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0254
Suprarenal gland	0.0124
Kidney	0.0121
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000
Breast	0.0340
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0082
Nerves	0.0020
Prostate	0.0205
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 112

	NORMAL % frequency	TUMOR % frequency	Ratio N/T	Ratio T/N
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Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0021	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0137	0.1542	6.4853
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0118	0.0043	0.0000	0.0000
Sensory organs	0.0043	0.0000	0.0000	0.0000
White blood cells	0.0000	0.0000	0.0000	0.0000
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0000
Gastrointestinal	0.0023	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 113

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0026	12.2035	0.0819
Breast	0.0102	0.0019	5.4442	0.1837
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0037	0.0031	1.1999	0.8334
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0020	2.0321	0.4921
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0180	0.0952	10.5060
Kidney	0.0017	0.0055	0.2991	3.3428
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0706			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0136
Gastrointestinal	0.0167	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0140
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0667	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 114

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N

Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0038	0.0000	undef
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0031	0.2400	4.1669
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0063	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
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Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0005
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 115

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0026	7.6272	0.1311
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0120	0.0052	2.3025	0.4343
Endocrine tissue	0.0068	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0007	0.0051	0.1440	6.9448
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0042	0.0137	0.3084	3.2426
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0055	0.0276	0.2393	4.1785
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0020
Placenta	0.0121	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 116

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0624	0.0204	3.0509	0.3278
Breast	0.0102	0.0000	undef	0.0000
Small intestine	0.0368	0.0165	2.2244	0.4496
Ovary	0.0120	0.0026	4.5050	0.2172
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0556	0.0000	undef	0.0000
Brain	0.0030	0.0041	0.7200	1.3890
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0190	0.0065	2.9412	0.3400
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0290	0.0230	1.2605	0.7933
Muscle-skeleton	0.0103	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0033	0.0110	0.2991	3.3428
Penis	0.1258	0.0000	undef	0.0000
Prostate	0.0479	0.0319	1.5013	0.6651
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.1067	0.0272	3.9279	0.2546
Uterus-general	0.0509	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0213			
Cervix				
FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency			
Development		Breast		
Gastrointestinal	0.0000	Ovary_n	0.0204	
Brain	0.0167	Ovary_t	0.1595	
Hematopoietic	0.0000	Endocrine tissue	0.0000	
Skin	0.0118	Fetal	0.0000	
Hepatic	0.0000	Gastrointestinal	0.0082	
Heart-blood vessels	0.0071	Hematopoietic	0.0610	
Lung	0.0000	Skin-muscle	0.0032	
Suprarenal gland	0.0000	Testicles	0.0000	
Kidney	0.0000	Lung	0.0000	
Placenta	0.0000	Nerves	0.0060	
Prostate	0.0499	Prostate	0.0342	
Sensory organs	0.0000	Sensory Organs	0.0000	
		Uterus_n	0.0541	

Electronic Northern for SEQ. ID NO.: 117

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0235			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

Electronic Northern for SEQ. ID NO.: 118

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0068	0.0150	0.4528	2.2083
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0051	0.1440	6.9448
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0064	0.0137	0.4626	2.1618
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0110	0.0000	undef
Penis	0.0044	0.0064	0.6824	1.4654
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0152	0.0063	2.2445	0.4455
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0039			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.1595
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0006
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0114
Lung	Skin-muscle	0.0065
Suprarenal gland	Testicles	0.0154
Kidney	Lung	0.0000
Placenta	Nerves	0.0020
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0077
	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 119

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0819	0.0383	2.1356	0.4682
Breast	0.0473	0.0320	1.4811	0.6752
Small intestine	0.0460	0.0331	1.3903	0.7193
Ovary	0.0539	0.0442	1.2190	0.8204
Endocrine tissue	0.0494	0.0652	0.7576	1.3199
Gastrointestinal	0.0805	0.0139	5.7984	0.1725
Brain	0.0451	0.0390	1.1557	0.8653
Hematopoietic	0.0374	0.0379	0.9881	1.0121
Skin	0.0367	0.0000	undef	0.0000
Hepatic	0.0190	0.0223	0.5882	1.7000
Heart	0.0382	0.0825	0.4626	2.1618
Testicles	0.0173	0.0117	1.4759	0.5775
Lung	0.0384	0.0184	2.0886	0.4788
Stomach-esophagus	0.0580	0.0537	1.0805	0.9255
Muscle-skeleton	0.0514	0.0240	2.1416	0.4669
Kidney	0.0489	0.0479	1.0156	0.9808
Pancreas	0.0330	0.0663	0.4986	2.0057
Penis	0.0359	0.0000	undef	0.0000
Prostate	0.0610	0.0617	0.9883	1.0118
Uterus-endometrium	0.2838	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0000	undef	0.0000
Uterus-general	0.0509	0.0000	undef	0.0000
Breast hyperplasia	0.2206			
Prostate hyperplasia	0.0773			
Seminal vesicle	0.0089			
Sensory organs	0.0353			
White blood cells	0.0737			
Cervix	0.0319			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency		
Development	0.0278	Breast	0.0340
Gastrointestinal	0.0361	Ovary_n	0.1595
Brain	0.0125	Ovary_t	0.0101
Hematopoietic	0.0157	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0233
Hepatic	0.0260	Gastrointestinal	0.0488
Heart-blood vessels	0.0818	Hematopoietic	0.0285
Lung	0.0325	Skin-muscle	0.0227
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0432	Lung	0.0164
Placenta	0.0303	Nerves	0.0261
Prostate	0.0000	Prostate	0.1163
Sensory organs	0.0126	Sensory Organs	0.0929
		Uterus_n	0.0416

Electronic Northern for SEQ. ID NO.: 120

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0052	0.0041	1.2599	0.7937
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0026	0.0000	undef	undef
White blood cells	0.0106	0.0000	undef	undef
Cervix				

FETUS % frequency

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0070
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 121

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0273	0.0051	5.3391	0.1873
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0059	0.0041	1.4399	0.6945
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0052	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0109	0.0085	1.2795	0.7815
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0167

Electronic Northern for SEQ. ID NO.: 122

	NORMAL % frequency	TUMOR % frequency	Normals/Tumor	Ratios N/T	T/N
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Bladder	0.0351	0.0077	4.5763	0.2185	
Breast	0.0077	0.0038	2.0416	0.4898	
Small intestine	0.0184	0.0000	undef	0.0000	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0017	0.0000	undef	0.0000	
Gastrointestinal	0.0115	0.0093	1.2425	0.8048	
Brain	0.0030	0.0021	1.4399	0.6945	
Hematopoietic	0.0013	0.0000	undef	0.0000	
Skin	0.0073	0.0000	undef	0.0000	
Hepatic	0.0095	0.0000	undef	0.0000	
Heart	0.0233	0.0000	undef	0.0000	
Testicles	0.0058	0.0000	undef	0.0000	
Lung	0.0021	0.0000	undef	0.0000	
Stomach-esophagus	0.0000	0.0077	0.0000	undef	
Muscle-skeleton	0.0103	0.0000	undef	0.0000	
Kidney	0.0054	0.0000	undef	0.0000	
Pancreas	0.0000	0.0055	0.0000	undef	
Penis	0.0599	0.0000	undef	0.0000	
Prostate	0.0131	0.0149	0.8774	1.1397	
Uterus-endometrium	0.0068	0.0000	undef	0.0000	
Uterus-myometrium	0.0152	0.0340	0.4489	2.2276	
Uterus-general	0.0407	0.0000	undef	0.0000	
Breast hyperplasia	0.0064				
Prostate hyperplasia	0.0059				
Seminal vesicle	0.0178				
Sensory organs	0.0118				
White blood cells	0.0000				
Cervix	0.0000				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0278	Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0391	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0060
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 123

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0390	0.0051	7.6272	0.1311
Breast	0.0064	0.0056	1.1342	0.8817
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0060	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0050	0.3396	2.9444
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0035	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0193	0.0077	2.5211	0.3967
Muscle-skeleton	0.0154	0.0060	2.5700	0.3891
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0210	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0272	0.5811	1.7821
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0000			

	FETUS % frequency
Development	0.0139
Gastrointestinal	0.0083
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0082
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 124

	NORMAL % frequency	TUMOR % frequency	RatioS N/T	Ratios T/N
Bladder	0.0195	0.0026	7.6272	0.1311
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0050	0.3398	2.9444
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0022	0.0021	1.0799	0.9260
Hematopoietic	0.0000	0.0379	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0060	0.0000	undef
Muscle-skeleton	0.0109	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0087	0.0043	2.0473	0.4885
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	-	-	-
Breast hyperplasia	0.0059	-	-	-
Prostate hyperplasia	0.0000	-	-	-
Seminal vesicle	0.0000	-	-	-
Sensory organs	0.0009	-	-	-
White blood cells	0.0000	-	-	-
Cervix	-	-	-	-

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0260	Gastrointestinal	0.0006
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0162
Suprarenal gland	0.0507	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 125

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder	0.0390	0.0051	7.6272	0.1311
Breast	0.0153	0.0150	1.0208	0.9796
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0210	0.0078	2.6863	0.3723
Endocrine tissue	0.0170	0.0125	1.3585	0.7361
Gastrointestinal	0.0153	0.0000	undef	0.0000
Brain	0.0126	0.0133	0.9415	1.0622
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0127	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0114	0.0143	0.7983	1.2526
Stomach-esophagus	0.0097	0.0307	0.3151	3.1733
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0326	0.0274	1.1890	0.8406
Pancreas	0.0033	0.0166	0.1994	5.0142
Penis	0.0629	0.0000	undef	0.0000
Prostate	0.0109	0.0170	0.6398	1.5531
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0068	4.4891	0.2228
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0256			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0191			
Cervix	0.0106			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
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Development	0.0000	Breast	0.0000
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0162
Suprarenal gland	0.0254	Testicles	0.0077
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0120
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0749

Electronic Northern for SEQ. ID NO.: 126

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0051	0.0056	0.9074	1.1021
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0060	0.0104	0.5756	1.7372
Endocrine tissue	0.0085	0.0075	1.1321	0.8833
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0059	0.0154	0.3840	2.6043
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0129	0.7353	1.3600
Heart	0.0201	0.0137	1.4649	0.6827
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0145	0.0164	0.8891	1.1248
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0017	0.0300	0.0571	17.5100
Kidney	0.0217	0.0068	3.1722	0.3152
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0210	0.0000	undef	0.0000
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0457	0.0204	2.2445	0.4455
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0470			
Sensory organs	0.0121			
White blood cells	0.0213			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0139
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0213
Lung	0.0217
Suprarenal gland	0.0254
Kidney	0.0185
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000
Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0210
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0259
Testicles	0.0000
Lung	0.0000
Nerves	0.0020
Prostate	0.0000
Sensory Organs	0.0387
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 127

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0090	0.0019	4.7637	0.2099
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0240	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0037	0.0010	3.5998	0.2778
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0058	0.0234	0.2460	4.0652
Lung	0.0010	0.0061	0.1693	5.9051
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0090	0.0000	undef	0.0000
Penis	0.0044	0.0064	0.6824	1.4654
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0229	0.0136	1.6834	0.5940
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0267			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0082
Placenta	Nerves	0.0010
Prostate	Prostate	0.0205
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0042

Electronic Northern for Seq. ID: 391

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0312	0.0000	undef 0.0000
Breast	0.0079	0.0056	1.4090 0.7097
Large intestine	0.0077	0.0000	undef 0.0000
Small intestine	0.0027	0.0107	0.2577 3.8812
Ovary	0.0030	0.0072	0.4148 2.4109
Endocrine tissue	0.0048	0.0089	0.5432 1.8409
Brain	0.0029	0.0080	0.3827 2.7574
Skin	0.0000	0.0000	undef undef
Hepatic	0.0093	0.0000	undef 0.0000
Heart	0.0020	0.0000	undef 0.0000
Testicles	0.0000	0.0118	0.0000 undef
Lung	0.0010	0.0037	0.2831 3.8007
Stomach-esophagus	0.0217	0.0000	undef 0.0000
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidney	0.0045	0.0048	0.9285 1.0770
Pancreas	0.0017	0.0055	0.2992 3.3427
Prostate	0.0066	0.0039	1.6882 0.5923
T lymphoma	0.0025	0.0149	0.1591 5.9152
Uterus	0.0000	0.0046	0.6428 1.5563
White blood cells	0.0021	0.0000	undef 0.0000
Hematopoietic	0.0000		
Penis	0.0134		
Seminal vesicle	0.0070		
Sensory organs	0.0070		

FETUS
% freq.

	0.0278
Development	0.0000
Gastrointestinal	0.0188
Brain	0.0079
Hematopoietic	0.0000
Skin	0.0260
Hepatic	0.0071
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0128
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0245
Gastrointestinal	0.0064
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0065
Testicles_t	0.0157
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0060
Ovary_Uterus	0.0000
Prostate_n	0.0050
Sensory organs	0.0182
White blood cells	0.0000

Electronic Northern for Seq. ID: 392

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0155	0.0000	0.0000
Breast	0.0000	0.0000	undef undef
Large intestine	0.0000	0.0000	undef undef
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0059	0.0000	undef undef
Endocrine tissue	0.0000	0.0000	0.0000
Brain	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0010	0.0000	0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Seminal vesicle	0.0000	0.0000	undef undef
Sensory organs	0.0000	0.0000	undef undef

FETUS
% freq.

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0010
Kidney_t	0.0000
Ovary_Uterus	0.0023
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 393

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T	T/N
B lymphoma	0.0075	0.0000	undef	0.0000
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0009	0.0000	undef	0.0000
Large intestine	0.0057	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	0.0000
Heart	0.0046	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	0.0000
Stomach-esophagus	0.0010	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	0.0000
Kidney	0.0034	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	0.0000
Prostate	0.0000	0.0055	0.0000	undef
T lymphoma	0.0000	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	0.0000
White blood cells	0.0000	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	0.0000
Penis	0.0027	0.0000	undef	0.0000
Seminal vesicle	0.0000	0.0000	undef	0.0000
Sensory organs	0.0000	0.0000	undef	0.0000

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0020
Kidney_t	0.0000
Ovary_Uterus	0.0045
Prostate_n	0.0000
Sensory_organisms	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 394

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T	T/N
B lymphoma	0.0000	0.0136	0.0000	undef
Bladder	0.0156	0.0023	6.6380	0.1505
Breast	0.0035	0.0042	0.8349	1.1977
Large intestine	0.0038	0.0199	0.1922	5.2023
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0059	0.0024	2.4887	0.4018
Endocrine tissue	0.0080	0.0000	undef	0.0000
Brain	0.0023	0.0040	0.5803	1.7234
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0030	0.0000	undef	undef
Testicles	0.0000	0.0053	0.0000	undef
Lung	0.0013	0.0055	0.3500	2.8506
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0045	0.0048	0.9285	1.0000
Pancreas	0.0033	0.0110	0.2992	3.3427
Prostate	0.0057	0.0026	2.1706	0.4607
T lymphoma	0.0051	0.0149	0.3381	2.3576
Uterus	0.0015	0.0000	undef	0.0000
White blood cells	0.0021	0.0304	0.0676	14.7861
Hematopoietic	0.0013			
Penis	0.0054			
Seminal vesicle	0.0000			
Sensory organs	0.0118			

FETUS
% freq.

	% freq.
Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0051
Fetal	0.0000
Gastrointestinal	0.0017
Hematopoietic	0.0122
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0231
Nerves	0.0000
Kidney_t	0.0040
Ovary_Uterus	0.0000
Prostate_n	0.0068
Sensory_organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 395

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
--	-------------------	------------------	-------------------

B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0156	0.0047	3.3192 0.3013
Breast	0.0062	0.0183	0.3372 2.9657
Large intestine	0.0019	0.0114	0.1682 5.9454
Small intestine	0.0000	0.0107	0.0000 undef
Ovary	0.0030	0.0072	0.4148 2.4110
Endocrine tissue	0.0000	0.0000	undef undef
Brain	0.0006	0.0010	0.6045 1.6542
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0190	0.0000 undef
Heart	0.0020	0.0962	0.0211 47.4018
Testicles	0.0000	0.0000	undef undef
Lung	0.0039	0.0111	0.3508 2.8506
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0171	0.0037	4.6389 0.2156
Kidney	0.0045	0.0000	undef 0.0000
Pancreas	0.0000	0.0110	0.0000 undef
Prostate	0.0000	0.0052	0.0000 undef
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0015	0.0000	undef 0.0000
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0013	0.0054	0.0000 undef
Penis	0.0000	0.0000	0.0000 0.0000
Seminal vesicle	0.0000	0.0000	0.0000 0.0000
Sensory organs	0.0000	0.0000	0.0000 0.0000

FETUS
% freq.

Development	0.0278
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0000
Ovary_Uterus	0.0113
Prostate_n	0.0000
Sensory_organisms	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 396

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0136	0.0000 undef
Bladder	0.0429	0.0000	undef 0.0000
Breast	0.0000	0.0042	0.0000 undef
Large intestine	0.0000	0.0000	0.0000 undef
Small intestine	0.0038	0.0000	undef 0.0000
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0000	0.0000	undef undef
Brain	0.0032	0.0000	undef 0.0000
Skin	0.0012	0.0010	1.1605 0.8617
Hepatic	0.0037	0.0000	undef 0.0000
Heart	0.0046	0.0000	undef 0.0000
Testicles	0.0051	0.0000	undef 0.0000
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0055	0.0000 undef
Muscle-skeleton	0.0000	0.0064	0.0000 undef
Kidney	0.0017	0.0037	0.4639 2.1557
Pancreas	0.0045	0.0000	undef 0.0000
Prostate	0.0017	0.0000	undef 0.0000
T lymphoma	0.0009	0.0026	0.3618 2.7643
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0030	0.0000	undef 0.0000
Hematopoietic	0.0007	0.0000	undef 0.0000
Penis	0.0000		
Seminal vesicle	0.0054		
Sensory organs	0.0000		
	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0075
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0084
Lungs_n	0.0000
Lungs_t	0.0098
Nerves	0.0000
Kidney_t	0.0070
Ovary_Uterus	0.0000
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	0.0077
	0.0000

Electronic Northern for Seq. ID: 397

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0117	0.0000	undef 0.0000
Breast	0.0009	0.0000	undef 0.0000
Large intestine	0.0000	0.0000	undef undef
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0030	0.0000	undef 0.0000
Endocrine tissue	0.0048	0.0000	undef 0.0000
Brain	0.0006	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0010	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0019	0.0018	1.0524 0.9502
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0009	0.0026	0.3618 2.7643
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0050	0.0000	undef undef
White blood cells	0.0007	0.0000	undef 0.0000
Hematopoietic	0.0000		
Penis	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0062
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0051
Fetal	0.0000
Gastrointestinal	0.0070
Hematopoietic	0.0122
Skin-muscle	0.0000
Testicles_n	0.0293
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0000
Ovary_Uterus	0.0135
Prostate_n	0.0061
Sensory_Organs	0.0000
White blood cells	0.0000

TRANSLATED BY SPSS

Electronic Northern for Seq. ID: 398

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0156	0.0023	6.6384 0.1506
Breast	0.0053	0.0042	1.2524 0.7985
Large intestine	0.0000	0.0028	0.0000 undef
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0030	0.0024	1.2443 0.8037
Endocrine tissue	0.0000	0.0057	0.0000 undef
Brain	0.0024	0.0060	0.4030 2.4814
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0030	0.0137	0.2215 4.5145
Testicles	0.0090	0.0000	undef 0.0000
Lung	0.0069	0.0037	1.8417 0.5430
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidney	0.0022	0.0000	undef 0.0000
Pancreas	0.0000	0.0055	0.0000 undef
Prostate	0.0028	0.0026	1.0853 0.9214
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0000	0.0092	0.0000 undef
White blood cells	0.0082	0.0000	undef 0.0000
Hematopoietic	0.0013		
Penis	0.0054		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS
% freq.

	0.0000
Development	0.0028
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0036
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0030
Kidney_t	0.0000
Ovary_Uterus	0.0090
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 399

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0136	0.0000 undef
Bladder	0.0234	0.0047	4.3788 0.2009
Breast	0.0070	0.0098	0.7157 1.3973
Large intestine	0.0057	0.0085	0.6729 1.4864
Small intestine	0.0110	0.0000	undef 0.0000
Ovary	0.0059	0.0000	undef 0.0000
Endocrine tissue	0.0032	0.0038	0.8479 1.1734
Brain	0.0018	0.0020	0.9068 1.1028
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0046	0.0190	0.2441 4.0960
Heart	0.0081	0.0000	undef 0.0000
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0068	0.0018	3.6834 0.2715
Stomach-esophagus	0.0072	0.0064	1.1333 0.8824
Muscle-skeleton	0.0069	0.0000	undef 0.0000
Kidney	0.0067	0.0096	0.6963 1.4362
Pancreas	0.0033	0.0221	0.1496 6.6857
Prostate	0.0094	0.0052	1.8088 1.5529
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0093	0.0000	undef 0.0000
White blood cells	0.0068	0.0000	undef 0.0000
Hematopoietic	0.0000		
Penis	0.0134		
Seminal vesicle	0.0070		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0408
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.1595
Endocrine tissue	0.0101
Fetal	0.0000
Gastrointestinal	0.0046
Hematopoietic	0.0122
Skin-muscle	0.0000
Testicles_n	0.0130
Testicles_t	0.0125
Lungs_n	0.0000
Lungs_t	0.0098
Nerves	0.0000
Kidney_t	0.0000
Ovary_Uterus	0.0000
Prostate_n	0.0068
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 400

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
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B lymphoma	0.0000	0.0136	0.0000 undef
Bladder	0.0156	0.0000	undef 0.0000
Breast	0.0018	0.0000	undef 0.0000
Large intestine	0.0000	0.0000	undef undef
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0000	0.0000	undef undef
Brain	0.0016	0.0019	0.8479 1.1794
Skin	0.0018	0.0010	1.8135 0.5514
Hepatic	0.0073	0.0000	undef 0.0000
Heart	0.0046	0.0000	undef 0.0000
Testicles	0.0020	0.0000	undef 0.0000
Lung	0.0040	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0033	0.0000	undef 0.0000
T lymphoma	0.0047	0.0026	1.8088 0.5529
Uterus	0.0025	0.0000	undef 0.0000
White blood cells	0.0031	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Seminal vesicle	0.0027	0.0000	undef undef
Sensory organs	0.0000	0.0000	undef undef

FETUS % freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0110
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0040
Kidney_t	0.0000
Ovary_Uterus	0.0045
Prostate_n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 401

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0125	0.0136	0.9198 1.0872
Bladder	0.0390	0.0094	4.1487 0.2410
Breast	0.0158	0.0056	2.8179 0.3549
Large intestine	0.0172	0.0028	6.0551 0.1652
Small intestine	0.0110	0.0000	undef 0.0000
Ovary	0.0178	0.0119	1.4932 0.6697
Endocrine tissue	0.0161	0.0195	0.8231 1.2150
Brain	0.0179	0.0170	1.0581 0.9451
Skin	0.0220	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0162	0.0275	0.5907 1.6929
Testicles	0.0161	0.0000	undef 0.0000
Lung	0.0175	0.0092	1.8944 0.5279
Stomach-esophagus	0.0000	0.0128	0.0000 undef
Muscle-skeleton	0.0257	0.0037	6.9583 0.1437
Kidney	0.0201	0.0096	2.0891 0.4787
Pancreas	0.0066	0.0276	0.2393 4.1784
Prostate	0.0104	0.0000	undef 0.0000
T lymphoma	0.0051	0.0448	0.1127 8.8727
Uterus	0.0177	0.0776	0.5426 1.5563
White blood cells	0.0116	0.0407	0.1916 5.2186
Hematopoietic	0.0040		
Penis	0.0241		
Seminal vesicle	0.0070		
Sensory organs	0.0353		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0157
Hematopoietic	0.0000
Skin	0.0269
Hepatic	0.0025
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0195
Kidney	0.1212
Placenta	0.0000
Prostate	0.0377
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0226
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0324
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0191
Kidney_t	0.0000
Ovary_Uterus	0.0248
Prostate_n	0.0061
Sensory Organs	0.0077
White blood cells	0.0000

Electronic Northern for Seq. ID: 402

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T	T/N
B lymphoma	0.0125	0.0000	undef	0.0000
Bladder	0.0429	0.0141	3.0424	0.3287
Breast	0.0387	0.0084	4.5922	0.2178
Large intestine	0.0038	0.0028	1.3456	0.7432
Small intestine	0.0165	0.0107	1.5459	0.6459
Ovary	0.0237	0.0000	undef	0.0000
Endocrine tissue	0.0177	0.0018	9.9589	0.1004
Brain	0.0041	0.0100	0.4062	2.4620
Skin	0.0514	0.0000	undef	0.0000
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0457	0.0137	3.3227	0.3010
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0467	0.0296	1.5796	0.6335
Stomach-esophagus	0.0145	0.0064	2.2671	0.4411
Muscle-skeleton	0.0171	0.0222	0.7731	1.2334
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Prostate	0.0075	0.0052	1.4470	0.6911
T lymphoma	0.0051	0.0000	undef	0.0000
Uterus	0.0281	0.0138	2.0348	0.4915
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0160			
Penis	0.0293			
Seminal vesicle	0.0141			
Sensory organs	0.0353			

FETUS
% freq.

Development	0.0418
Gastrointestinal	0.0139
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0325
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0121
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.2475
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0220
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0583
Testicles_n	0.0442
Testicles_t	0.0000
Lungs_n	0.0998
Lungs_t	0.0000
Nerves	0.0090
Kidney_t	0.0000
Ovary_Uterus	0.0405
Prostate_n	0.0061
Sensory_organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 403

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0351	0.0047	7.4677 0.1339
Breast	0.0070	0.0014	5.0097 0.1396
Large intestine	0.0115	0.0000	undef 0.0000
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0024	0.0000 undef
Endocrine tissue	0.0016	0.0035	0.4527 2.2091
Brain	0.0017	0.0060	0.2901 3.4467
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0020	0.0137	0.1477 6.7715
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0039	0.0018	2.1049 0.4751
Stomach-esophagus	0.0145	0.0000	undef 0.0000
Muscle-skeleton	0.0051	0.0000	undef 0.0000
Kidney	0.0112	0.0000	undef 0.0000
Pancreas	0.0017	0.0055	0.2392 3.3427
Prostate	0.0075	0.0026	2.8941 0.3455
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0059	0.0046	1.2851 0.7781
White blood cells	0.0027	0.0000	undef 0.0000
Hematopoietic	0.0013		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0254
Kidney	0.0189
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0340
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0998
Lungs_t	0.0000
Nerves	0.0020
Kidney_t	0.0000
Ovary_Uterus	0.0000
Prostate_n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

2.2. Fisher Test

In order to decide whether a partial sequence S of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to S. If the null hypothesis can be rejected with high enough certainty, the gene belonging to S is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

Example 3

Automatic Lengthening of the Partial Sequence

Automatic lengthening of partial sequence S is completed in three steps:

1. Determination of all sequences homologous to S from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence C from the assembled sequences.

Consensus sequence C will generally be longer than initial sequence S. Its electronic Northern Blot will accordingly

deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences C_i (i : iteration index) obtained in each case until the alternative hypothesis is rejected (if H_0 Exit; truncation criterion I) or until automatic lengthening is no longer possible (while $C_i > C_{i-1}$; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from normal bladder tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORF's) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

TOP SECRET - DRAFT

Example 4**Mapping of Nucleic Acid Sequences on the Human Genome**

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server (http://www.stanford.edu/RH/rhserver_form2.html). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

Example 5

Obtaining genomic DNA sequences (BAC clones)

The genomic BAC clones containing the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well". In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clones, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries used were CITB B and CITB C:

Sed. ID No.	Identified BACs		
60	311/K/13	271/E/3	252/P/20
102	458/N/24	349/F/12	

TABLE I

Col. 1 - Sequence ID

Col. 2 - Expression

Col. 3 - Function

Col. 4 - Modules

Col. 5 - Cytogenetic localization

Col. 6 - Nearest marker

TABLE I

Sequence ID	Expression	Function
1	Overexpressed in normal bladder tissue	H. sapiens rap1b
2	Overexpressed in normal bladder tissue	Human zinc finger transcription factor hEZF (EZF) homolog
3	Overexpressed in normal bladder tissue	Homo sapiens mRNA for phosphatidic acid phosphatase 2a
4	Overexpressed in normal bladder tissue	H. sapiens mRNA for G protein-coupled receptor Edg-2
6	Overexpressed in normal bladder tissue	Homo sapiens secreted frizzled-related protein
7	Overexpressed in normal bladder tissue	Human monocytic leukemia zinc finger protein (MOZ)
8	Overexpressed in normal bladder tissue	Homo sapiens angiotensin II receptor
9	Overexpressed in normal bladder tissue	Human mRNA for RNA helicase (HRH1)
12	Overexpressed in normal bladder tissue	H. sapiens rhoB
13	Overexpressed in normal bladder tissue	Human skeletal muscle LIM-protein SLIM 1
14	Overexpressed in normal bladder tissue	Homo sapiens 39 kDa protein
17	Overexpressed in normal bladder tissue	H. sapiens dermatopontin mRNA
18	Overexpressed in normal bladder tissue	Homo sapiens phosphoglucomutase-related protein (PGMRP)

20	Overexpressed in normal bladder tissue	Human nucleic acid binding protein CNBP
21	Overexpressed in normal bladder tissue	Unknown
22	Overexpressed in normal bladder tissue	Human small nuclear ribonucleoprotein (U1-70K)
23	Overexpressed in normal bladder tissue	H. sapiens mRNA for telokin homolog
24	Overexpressed in normal bladder tissue	Homologous to pil2 from rats
25	Overexpressed in normal bladder tissue	Unknown
26	Overexpressed in normal bladder tissue	Unknown
27	Overexpressed in normal bladder tissue	Unknown
29	Overexpressed in normal bladder tissue	Homologous to sushi repeat protein
30	Overexpressed in normal bladder tissue	Unknown
31	Overexpressed in normal bladder tissue	Unknown
32	Overexpressed in normal bladder tissue	Unknown
33	Overexpressed in normal bladder tissue	Unknown
34	Overexpressed in normal bladder tissue	Unknown

35	Overexpressed in normal bladder tissue	Caenorhabditis elegans cosmid F09E5
36	Overexpressed in normal bladder tissue	Unknown
37	Overexpressed in normal bladder tissue	Homologous to murine RING zinc finger protein
38	Overexpressed in normal bladder tissue	Rattus norvegicus cytoplasmic dynein intermediate chain 2c
39	Overexpressed in normal bladder tissue	Unknown
40	Overexpressed in normal bladder tissue	Unknown
43	Overexpressed in normal bladder tissue	Gry-rbp
44	Overexpressed in normal bladder tissue	Unknown
46	Overexpressed in normal bladder tissue	Unknown
47	Overexpressed in normal bladder tissue	Unknown
48	Overexpressed in normal bladder tissue	Unknown
50	Overexpressed in normal bladder tissue	Homologous to HU-K5
51	Overexpressed in normal bladder tissue	Unknown
52	Overexpressed in normal bladder tissue	Homologous to O. aries putative G- protein linked receptor (edg-2)

53	Overexpressed in normal bladder tissue	Unknown
54	Overexpressed in normal bladder tissue	Human homolog to murine NST-1
55	Overexpressed in normal bladder tissue	Homologous to human CIP4
56	Overexpressed in normal bladder tissue	Human Cbf5p homolog
57	Overexpressed in normal bladder tissue	Unknown
58	Overexpressed in normal bladder tissue	Unknown
59	Overexpressed in normal bladder tissue	Unknown
60	Overexpressed in normal bladder tissue	Unknown
61	Overexpressed in normal bladder tissue	Caenorhabditis elegans cosmid TC9A5
62	Overexpressed in normal bladder tissue	Unknown
63	Overexpressed in normal bladder tissue	Unknown
65	Overexpressed in normal bladder tissue	Homologous to human KOX15
67	Overexpressed in normal bladder tissue	Unknown
69	Overexpressed in normal bladder tissue	Homologous to Golgi 4-transmembrane spanning transporter MTP

72	Overexpressed in normal bladder tissue	Unknown
73	Overexpressed in normal bladder tissue	Unknown
75	Overexpressed in normal bladder tissue	Human homolog to rat mRNA for V-1 protein
77	Overexpressed in normal bladder tissue	Caenorhabditis elegans cosmid F 13G3
78	Overexpressed in normal bladder tissue	Unknown
79	Overexpressed in normal bladder tissue	Unknown
80	Overexpressed in normal bladder tissue	Human pyruvate dehydrogenase kinase isoform 4
82	Overexpressed in normal bladder tissue	Unknown
83	Overexpressed in normal bladder tissue	Unknown
85	Overexpressed in normal bladder tissue	Unknown
86	Overexpressed in normal bladder tissue	Mouse epithelial zinc-finger protein EZF (Zie)
88	Overexpressed in normal bladder tissue	Unknown
90	Overexpressed in normal bladder tissue	Unknown
92	Overexpressed in normal bladder tissue	Homologous to MyD118

PROTEIN IDENTIFIED

93	Overexpressed in normal bladder tissue	Homologous to p8 protein from rats
94	Overexpressed in normal bladder tissue	Unknown
95	Overexpressed in normal bladder tissue	Unknown
96	Overexpressed in normal bladder tissue	Homologous to murine B-1ND1
97	Overexpressed in normal bladder tissue	Canis familiaris Sec61-complex gamma-subunit
98	Overexpressed in normal bladder tissue	Unknown
99	Overexpressed in normal bladder tissue	Human homolog to X taevis 146 kDa nuclear protein
100	Overexpressed in normal bladder tissue	Unknown
101	Overexpressed in normal bladder tissue	Human dysferlin
102	Overexpressed in normal bladder tissue	Unknown
103	Overexpressed in normal bladder tissue	Unknown
104	Overexpressed in normal bladder tissue	Unknown
105	Overexpressed in normal bladder tissue	Unknown
106	Overexpressed in normal bladder tissue	Unknown

UNPUBLISHED DATA

107	Overexpressed in normal bladder tissue	Unknown
108	Overexpressed in normal bladder tissue	Homologous to APRIL
109	Overexpressed in normal bladder tissue	Homologous to the human p20
110	Overexpressed in normal bladder tissue	Unknown
111	Overexpressed in normal bladder tissue	Unknown
112	Overexpressed in normal bladder tissue	Unknown
113	Overexpressed in normal bladder tissue	Homologous to <i>D. melanogaster</i> furrowed
114	Overexpressed in normal bladder tissue	Homologous to murine BRX protein
115	Overexpressed in normal bladder tissue	Unknown
116	Overexpressed in normal bladder tissue	Unknown
117	Overexpressed in normal bladder tissue	<i>Caenorhabditis elegans</i> cosmid R08D7
118	Overexpressed in normal bladder tissue	Unknown
119	Overexpressed in normal bladder tissue	HSP 86
120	Overexpressed in normal bladder tissue	Homologous to human AKAP95

121	Overexpressed in normal bladder tissue	Sus scrofa mRNA for 17-kDa PKC-potentiated inhibitory protein of PP1
122	Overexpressed in normal bladder tissue	Unknown
123	Overexpressed in normal bladder tissue	Homo sapiens supervillin
124	Overexpressed in normal bladder tissue	Homologous to B. taurus vacuolar ATPase subunit A
125	Overexpressed in normal bladder tissue	SH3 domain binding glutamic acid-rich-like protein
126	Overexpressed in normal bladder tissue	Human homolog to Mus musculus WSB-1
127	Overexpressed in normal bladder tissue	Unknown
391	Lengthening to Seq. ID No: 27	
392	Lengthening to Seq. ID No: 34	
393	Lengthening to Seq. ID No: 50	
394	Lengthening to Seq. ID No: 56	
395	Lengthening to Seq. ID No: 78	
396	Lengthening to Seq. ID No: 82	
397	Lengthening to Seq. ID No: 88	
398	Lengthening to Seq. ID No: 100	
399	Lengthening to Seq. ID No: 101	

400	Lengthening to Seq. ID No: 102	
401	Lengthening to Seq. ID No: 104	
402	Lengthening to Seq. ID No: 110	
403	Lengthening to Seq. ID No: 111	

[Key to Table I:]

[Column 4: Sequence ID No. 109:] crystallin = crystalline

[Column 6: Sequence ID Nos. 6, 7, 9, 22, 29, 31-34, 39, 43, 46,
48, 50, 51, 56, 58-62, 65, 72, 73, 82, 86, 102,
103, 111, 112, 115, 126:] ... bis ... = ... to ...

TABELLE I

Sequenz Expression ID	Funktion	Module	Cytoxygenetische Lokalisation	Nearest Marker
1 in Blasennormalgewebe überexprimiert	H.sapiens rap 1b	ras	6q21-q22.1	D6S304-D6S1639
2 in Blasennormalgewebe überexprimiert	Human zinc finger transcription factor HEZF (EZF Homolog)	ZINC_FINGER_C2H2_2		
3 in Blasennormalgewebe überexprimiert	Homo sapiens mRNA for phosphatidic acid phosphatase 2a		9q31.3-q32	D9S1690-D9S279
4 in Blasennormalgewebe überexprimiert	H. sapiens mRNA for G protein-coupled receptor Egfr-2	FZ DOMAIN_NETRIN_C7; PRO_RICH	8p11.23-p12	SHGC-5722 bis SHGC-5765
6 in Blasennormalgewebe überexprimiert	Homo sapiens secreted frizzled-related protein		8p11.23-p12	D8S2070 bis SHGC-31558
7 in Blasennormalgewebe überexprimiert	Human monocytic leukaemia zinc finger protein (MOZ)		22q11.22-q11.23	D6S2136-D4S3274
8 in Blasennormalgewebe überexprimiert	Homo Sapiens angiotensin II receptor		6p21.31	SHGC-17229 bis D6S478
9 in Blasennormalgewebe überexprimiert	Human mRNA for RNA helicase (HRH1)		2p23.3	D2S387
12 in Blasennormalgewebe überexprimiert	H. sapiens rhoB			
13 in Blasennormalgewebe überexprimiert	Human skeletal muscle LM-protein SLIM1	LIM DOMAIN_2	Xq25-q27.2	DIXS94-DXS1062
14 in Blasennormalgewebe überexprimiert	Homo sapiens 39 kDa protein	PDZ_LIM	4q34.1-q35.2	D4S408-D4S426
17 in Blasennormalgewebe überexprimiert	H. sapiens dermatopontin mRNA		1q23.1-q23.2	D1S445;D1S2750
18 in Blasennormalgewebe überexprimiert	Homo sapiens phosphoglycanutase-related protein (PGMRP)	PGM_PMM	9p11.1-q12	D9S1699
20 in Blasennormalgewebe überexprimiert	Human nucleic acid binding protein CNBP	Zf-CCHC	3q13.31-q21.1	D3S1689-D3S1786
21 in Blasennormalgewebe überexprimiert	unbekannt			
22 in Blasennormalgewebe überexprimiert	Human small nuclear ribonucleoprotein (U1-70K)		19q13.31-q13.33	SHGC-36947 bis SHGC-34723
23 in Blasennormalgewebe überexprimiert	H.sapiens_mRNA for telokin Homolog			
24 in Blasennormalgewebe überexprimiert	Homolog zu p12 aus Ratte			

Tabelle 2: Tissue specific

Sequenz Expression ID	Funktion	Module	Cytogenetische Lokalisation	Nearest Marker
25	in Blasennormalgewebe unbekannt überexprimiert			
26	in Blasennormalgewebe unbekannt überexprimiert			
27	in Blasennormalgewebe unbekannt überexprimiert		5q32-q33.1	D5S470
29	in Blasennormalgewebe Homolog zu sushi repeat protein überexprimiert	PRO_RICH	3q11.2	SHGC-36351 bis SHGC-14633
30	in Blasennormalgewebe unbekannt überexprimiert		2q37.3	D2S206-D2S331
31	in Blasennormalgewebe unbekannt überexprimiert		2q31.1-q31.3	Wt-7596 bis D2S326
32	in Blasennormalgewebe unbekannt überexprimiert		20p13	D20S864 bis SHGC-34269
33	in Blasennormalgewebe unbekannt überexprimiert		13q12.11-q12.3	SHGC-2665 bis D13S289
34	in Blasennormalgewebe unbekannt überexprimiert		9q21.31	SHGC-32247 bis SHGC-5528
35	in Blasennormalgewebe Caenorhabditis elegans cosmid F09E5 überexprimiert	UPF0001		
36	in Blasennormalgewebe unbekannt überexprimiert			
37	in Blasennormalgewebe Homolog zu murine RING zinc finger überexprimiert	PRO_RICH_ZF_RING	17p13.3	D17S1548
38	in Blasennormalgewebe Rattus norvegicus cytoplasmic dynein überexprimiert	WD40_REGION	10q11.21	D10S604-D10S220
39	in Blasennormalgewebe intermedia chain 2c überexprimiert		13q33.3	SHGC-9496 bis D13S1223
40	in Blasennormalgewebe unbekannt überexprimiert			
43	in Blasennormalgewebe Gyr-tbp überexprimiert	RBD	20p13	D20S816 bis SHGC-33687
44	in Blasennormalgewebe unbekannt überexprimiert			
46	in Blasennormalgewebe unbekannt überexprimiert		2q21.3-q22.1	SHGC-35092 bis SHGC-32856
47	in Blasennormalgewebe unbekannt überexprimiert			

Sequenz ID	Expression	Funktion	Module	Cytozentrische Lokalisation	Nearest Marker
48	in Blasennormalgewebe überexprimiert	unbekannt		15q11.2-q15.3	SHGC-35142 bis SHGC-7407
50	in Blasennormalgewebe überexprimiert	Homolog zu HU-K5		3q21.3-3q23	SHGC-37132 bis SHGC-30693
51	in Blasennormalgewebe überexprimiert	unbekannt		3p21.31-p21.1	SHGC-30574 bis SHGC-31529
52	in Blasennormalgewebe überexprimiert	Homolog zu O. aries Putative G-protein linked receptor (edg-2)			
53	in Blasennormalgewebe überexprimiert	unbekannt			
54	in Blasennormalgewebe überexprimiert	Humanes Homolog zu murinem NST-1	HSP70		
55	in Blasennormalgewebe überexprimiert	Homolog zu humanem CIP4			
56	in Blasennormalgewebe überexprimiert	Humanes Chifsp Homolog	ZF_DHHC; NLS_BP	Xq25-q27.3	SHGC-31168 bis AFM207x08
57	in Blasennormalgewebe überexprimiert	unbekannt		9q12	WI_7387 bis SHGC-32868
58	in Blasennormalgewebe überexprimiert	unbekannt		9q22.2-q22.31	SHGC-14680 bis SHGC-8725.
59	in Blasennormalgewebe überexprimiert	unbekannt			
60	in Blasennormalgewebe überexprimiert	unbekannt		1p36.13-p36.31	SHGC-34104 bis SHGC-9861
61	in Blasennormalgewebe überexprimiert	Caenorhabditis elegans cosmid T09A5		SHGC-2758 bis SHGC-4278	
62	in Blasennormalgewebe überexprimiert	unbekannt		Chr.5	
63	in Blasennormalgewebe überexprimiert	unbekannt	Oxysterol_BP	1q32.3	SHGC-15949 bis SHGC-11476
65	in Blasennormalgewebe überexprimiert	Homolog zu humanem K0X15	ZINC_FINGER_C2H2_2	D1S187-D1S417	D16S2624 bis SHGC-9008
67	in Blasennormalgewebe überexprimiert	unbekannt		1p32.3-p33	D8S566-D8S266
69	in Blasennormalgewebe überexprimiert	Homolog zu Cogl-4-Transmembran spanning Transporter MTP			SHGC-14535 bis SHGC-30780
72	in Blasennormalgewebe überexprimiert	unbekannt		10q23.1	

Sequenz Expression ID	Funktion	Module	Cytozentrische Lokalisation	Nearest Marker
73 in Blasennormalgewebe überexprimiert	unbekannt		1q22	SHGC-32289 bis D1S1576
75 in Blasennormalgewebe überexprimiert	Humanes Homolog zu Rat mRNA für V-1 protein	ank		
77 in Blasennormalgewebe überexprimiert	Caenorhabditis elegans cosmid F13G3	Ribosomal L13	8q23.3-q24.11	WI-5098, CHLC.GATABG03.443
78 in Blasennormalgewebe überexprimiert	unbekannt	lg		
79 in Blasennormalgewebe überexprimiert	unbekannt			
80 in Blasennormalgewebe überexprimiert	Humanne Pyruvate Dehydrogenase Kinase Isoform 4		7q21.2-q22.1	D7S492-D7S652
82 in Blasennormalgewebe überexprimiert	unbekannt		3p24.3-p23	SHGC-9648 bis SHGC-14769
83 in Blasennormalgewebe überexprimiert	unbekannt		3p12.1-p21.1	D3S3117
85 in Blasennormalgewebe überexprimiert	unbekannt			
86 in Blasennormalgewebe überexprimiert	Mouse epithelial zinc-finger protein EZF (Zif)		9q22.33-q31.1	D9S1690 bis SHGC-14345
88 in Blasennormalgewebe überexprimiert	unbekannt		1p35.1	D1S2569-D1S2876
90 in Blasennormalgewebe überexprimiert	unbekannt			
92 in Blasennormalgewebe überexprimiert	Homolog zu MyD118			
93 in Blasennormalgewebe überexprimiert	Homolog zum p8 Protein aus Ralle	ras	16p11.2-q12.1	D16S3093-D16S409
94 in Blasennormalgewebe überexprimiert	unbekannt		14q11.1-q11.2	D14S990-D14S264
95 in Blasennormalgewebe überexprimiert	unbekannt		16p13.2-p13.3	D16S521
96 in Blasennormalgewebe überexprimiert	Homolog zu murinam B-IND1		15q22.31-q22.33	D15S159-D15S125
97 in Blasennormalgewebe überexprimiert	Canis familiaris Sec61-complex gamma subunit	SecE		
98 in Blasennormalgewebe überexprimiert	unbekannt		6p21.2-p21.31	D6S276-D6S439

Sequenz Expression ID	Funktion	Module	Cytoge netische Lokalisation	Near esti marker
99 in Blasen normalgewebe über exprimiert	Humanes Homolog zu X laevis 146 kDa nuclear protein		2q23.3-q33.3	D2S117-D2S115
100 in Blasen normalgewebe über exprimiert	unbekannt	NLS_BP	9q22.31-q31.1	D9S176-D9S277
101 in Blasen normalgewebe über exprimiert	Humanes Dysferlin	PRO_RICH; C2_DGMAN_2		
102 in Blasen normalgewebe über exprimiert	unbekannt		10q25.3	D10S216 bis SHGC-13269
103 in Blasen normalgewebe über exprimiert	unbekannt		2p23.1-p23.2	D2S2573 bis SHGC-15275
104 in Blasen normalgewebe über exprimiert	unbekannt	PRO_RICH	8p11.23-p12	D8S2102
105 in Blasen normalgewebe über exprimiert	unbekannt		1p31.1-p34.1	SHGC-32050
106 in Blasen normalgewebe über exprimiert	unbekannt		13q21.33-q22.1	D13S156-D13S162
107 in Blasen normalgewebe über exprimiert	unbekannt			
108 in Blasen normalgewebe über exprimiert	Homolog zu APRIL	TNF		
109 in Blasen normalgewebe über exprimiert	Homolog zu dem humanen p20	crystallin; HSPB20	19q13.13	D10S425-D10S224
110 in Blasen normalgewebe über exprimiert	unbekannt		7q31.31	D7S522-D7S2756
111 in Blasen normalgewebe über exprimiert	unbekannt		10q23.31-q24.1	WI-7008 bis SHGC-34547
112 in Blasen normalgewebe über exprimiert	unbekannt		1q31.1-q31.3	SHGC-34113 bis SHGC-34344
113 in Blasen normalgewebe über exprimiert	Homolog zu D. melanogaster furrowed sushi		9q31.3-q32	D9S160-D9S279
114 in Blasen normalgewebe über exprimiert	Homolog zu murinem BRX Protein	PRO_RICH		
115 in Blasen normalgewebe über exprimiert	unbekannt			Chr.17 (17p13.3-q25.3)
116 in Blasen normalgewebe über exprimiert	unbekannt		4q28.1-q31.1	D4S1580-D4S427
117 in Blasen normalgewebe über exprimiert	Caenorhabditis elegans cosmid R08D7			

Sequenz Expression ID	Funktion	Module	Cyto/Genetische Lokalisation	Nearest Marker
118	In Blasennormalgewebe unbekannt	PRO_RICH		
119	In Blasennormalgewebe überexprimiert	HSP_86	HSP90	11q13.2-q13.5
120	In Blasennormalgewebe überexprimiert	Homolog zu humanem AKAP95	PRO_RICH	D11S913-D11S1314
121	In Blasennormalgewebe überexprimiert	Sus scrofa mRNA for 17-kDa PKC-related inhibitory protein of PP1	PRO_RICH	D19S1069-D19S421
122	In Blasennormalgewebe überexprimiert	unbekannt	PRO_RICH	D1S306-D1S2570
123	In Blasennormalgewebe überexprimiert	Homo sapiens Supervillin	PRO_RICH	1q32.1
124	In Blasennormalgewebe überexprimiert	Homolog zu <i>B. taurus</i> vacuolar ATPase subunit A	PRO_RICH	3q11.2-q21.1
125	In Blasennormalgewebe überexprimiert	SH3 domain binding glutamic acid-rich-like protein	binding	D3S2353-D3S3526
126	In Blasennormalgewebe überexprimiert	Humanes Homolog zu <i>Mus musculus</i> <td>WD40_REGION; WD40_SOCS_DOMAIN</td> <td>D17S783 bis SHGC-30289</td>	WD40_REGION; WD40_SOCS_DOMAIN	D17S783 bis SHGC-30289
127	In Blasennormalgewebe überexprimiert	unbekannt		
391	Verlängerung zu Seq ID No. 27			
392	Verlängerung zu Seq ID No. 34			
393	Verlängerung zu Seq ID No. 50			
394	Verlängerung zu Seq ID No. 56			
395	Verlängerung zu Seq ID No. 78			
396	Verlängerung zu Seq ID No. 82			
397	Verlängerung zu Seq ID No. 88			
398	Verlängerung zu Seq ID No. 100			
399	Verlängerung zu Seq ID No. 101			

Sequenz Expression ID	Funktion	Module	Cytogenetische Lokalisation	Nearest Marker
400	Verlängerung zu Seq ID No. 102			
401	Verlängerung zu Seq ID No. 104			
402	Verlängerung zu Seq ID No. 110			
403	Verlängerung zu Seq ID No. 111			

TABLE II

Seq. ID No.	Peptide Sequences (ORF's)	Seq. ID. No.

Seq. ID. No.	Peptid-Sequenzen (ORF's)	Seq. ID. No.
21		430 431
24		128 129
25		131 132 133
26		134 135 136
27		137 138 139
29		143
30		144 145 146 147 148
31		149 150 151 152
32		153 154 155
33		156 157
34		158 159 160
35		161 162 163
36		164 165 166
37		167
38		168
39		169
		170
		171
40		172 173 174
43		181
44		182 183 184

Seq. ID No. **Peptide Sequences (ORF's)** **Seq. ID. No.**

Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
46	188 189 190
47	191 192 193
48	194 195 196
50	200 201 202
51	203 204 205
52	206 207 208
53	209
54	210
55	211
56	212 213 214
57	215
58	216 217 218
59	219
60	220 221 222 223
61	224 225
62	226 227 228
63	229
65	233
67	237 238 239
69	243 244
72	251 252 253
73	254 255 256
75	260
77	264

Seq. ID No. **Peptide Sequences (ORF's)** **Seq. ID. No.**

Seq. ID. No.	Peptid-Sequenzen (ORF's)	Seq. ID. No.
78		265
		266
79		267
80		268
		269
		270
82		274
		275
		276
83		277
		278
		279
85		283
		284
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86		286
		287
		288
88		292
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		294
90		298
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92		304
93		305
		306
94		307
95		308
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		310
96		311
		312
97		313
		314
		315
98		316
		317
		318
99		319
100		320
		321
101		322
102		323
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		325
103		326
		327
		328
104		329
		330
		331
105		332
		???

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Seq. ID No. **Peptide Sequences (ORF's)** **Seq. ID. No.**

Seq. ID. No.	Peptid-Sequenzen (ORF's)	Seq. ID. No.
106		334 335 336
107		337 338 339
108		340 341 342
109		343 344 345
110		346 347
111		348 349 350
112		351 352 353
113		354
114		355 356 357
115		358 359 360
116		361 362 363 364
117		365 366 367
118		368 369 370
119		371 372
120		373 374
121		375
122		376 377
122		378
123		379 380 381
124		382 383 384
125		385 386 387

Seq. ID No.	Peptide Sequences (ORF's)	Seq. ID. No.
Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.	
126		388
127		389
		390
391		404
		405
392		406
		407
393		408
		409
394		410
		411
395		412
		413
396		414
		415
397		416
		417
398		418
		419
399		420
		421
400		422
		423
401		424
		425
402		426
		427
403		428
		429

(100-1000)

The inventive nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 128-390 and 404-431 are described in the following sequence protocol.

Sequence Protocol**(1) GENERAL INFORMATION:****(i) APPLICANT:**

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Normal Bladder Tissue

(iii) Number of sequences: 365

(iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

(2) INFORMATION ON SEQ ID NO. 1:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1722 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

(2) INFORMATION ON SEQ ID NO. 2:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1187 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

cggtctggagg	aggccggatcc	ttagtgtcacc	cacttgggcg	ctggacccccc	tctcagcaat	60
ggccacccggc	cggtctggaca	cgactttcccc	ctggggccgc	actcccccgc	aggactaccc	120
cgacccctggg	tttttgaggaa	gtgttgtggca	gcaggggactg	tcacccctgcc	ctgcggcttc	180
ctcccggtt	ccatccccac	cggggggcca	attacccttc	tttctctggcc	gateagatgc	240
agcccaagaat	cccgccgcgc	cattaccaag	agtcatacgcc	acccggttcc	tgcatacgcc	300
aggaggcccaat	gccaataggg	ggaaaggacat	ctgtggcccg	aaaaaggacc	gcacccacaca	360
cttttgttatta	cgccgggtgc	ggccaaaaatct	acacaaaagag	ttcccatatc	aaggcacacc	420
ttggaaaccca	cacaggttag	aaacaccttacc	actgtgactg	ggacggctgt	ggatggaaat	480
tcgcggcgtc	atgttgcgtt	accaggcaact	accgttaaca	cacggggcac	cgcccggttcc	540
agtgcacaaa	atgcgaccga	gcattttcca	ggtcggacca	ccttcgttta	cacatgaaga	600
ggcattttta	aatcccccac	agtgtatgtat	acccacactg	ccagaaggaga	attcgtatt	660
ttttactttt	cacatgttcc	ttccatgttgc	ggaaaggagcc	cagccagaaa	gcactacaat	720
catgttcaag	ttcccaacttgc	agtcatattttgc	tgatgtgata	atcggaaaa	atgaggaatc	780
aaaaagacaa	aaatcaaga	acatgtgggg	tcttgtgactg	gatcttttat	catttcaatt	840
ctaataccgc	cttggatattt	cattgttttttt	caaaatgtcca	agggggttgc	tggaaatgtt	900
ggatatacgg	gtatataat	tatccgttgc	tttggggagg	aaagaccaga	attcccttgc	960
atttgttattt	gtatgtat	aagcataaaa	gatcaccttgc	tatttttttgc	acccctttaaa	1020
agccattttt	atgttgttag	aaaaaggagg	agaatccatgc	gtacagaaaa	ccatgtttaa	1080
ataggccataat	gtatgttttttgc	gtggatcttgc	tcttaaagggt	cccaaaagg	gagccaaagg	1140
ttttaaacttgc	tggatcttgc	gcaaggggaa	atctgtgtttt	ttttccg		1187

(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1478 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

gccaaccgcg gggctggccg gtccctcgct gcccagcggg agggggctgga ccccgcggtc 60
 ctccccctctt ccgggttcacca tcccttaaaaagg gagatgttcgg acggcccgccg tggtggagag 120
 agccggccggg tccggacggg gggacaaacggg ggccaggccgt gggcggtcg gagggttcgg 240
 ggatcacagag ctggcccgccg tggcacacga gggccgtttccggc actaacccggg tgttcgccgg 300
 ggctgtgagg ggaggggcccc gggggccatt ggtggccgtgg ggaggccggcc cgccgttcgg 360
 cccggccctcg gtgtccctcc tccctcggtt gggggggggc ggtatcgcc ggtatcgccca
 gccccggccc gggctcgaga atcaaggggcc tcggccgccc tcccgcaagt Cagttccatcg 420
 cccttgcgggg ggacggccggg gagagggccat gtttgcacaatgg acggccgtccg ctgcgttcgg 480
 cttctggatgt ctgttcgtgt tggtggctgg atttccctttt gcaattttt cttcaaggaa 540
 taccccccttc caacggaggag tattctgtaa tgatgtatcc atcaaggatcc ttacaaaaaga 600
 agacaccata cttatgtatcc tattatgttg aataatccat ccattatgtt ttatccatgtat 660
 tattttttggaa gaaaaatctgt ctgtttactgt tttttttttt cttttttttt cttttttttt 720
 gaataactac atagccacta ttacaaaagg ctttggaaacc tttttttttt tgccagttcc 780
 tagtccatgg ctgtatgtaca ttggccaaatgt tttcaataggc agactcgccg ctactatctt 840
 ggatgtttgt gatccggatt ggtttttttt cttttttttt cttttttttt cttttttttt 900
 catatgttca ggaatgtcag aaaggtttaa ggaaggccgg tttttttttt attcaggccaa 960
 ctctttcggtt tccatgtact gcatgttccgtt tttttttttt tttttttttt cttttttttt 1020
 gggatgttgg gcaagactt ctggcccccac atggcaatctt ggtttttttt cttttttttt cttttttttt 1080

 ttatgtggc cttttctcgat ttcttgcattt taacaccac tggagccgtat tggtgtactgg 1140
 actcatccat ggagcttcgtt ttgcataatatt agttgtgtat tgatgtatccg attttttttttt 1200
 agaaagaact tttttttttttaaaaagg aaagaaaaaa ggaggactctt cttttttttt cttttttttt 1260
 accaaacaact gggaaatcaat atccggccaa tttttttttt cttttttttt cttttttttt 1320
 agggttgaatctt ggcctgtttt cttttttttt cttttttttt cttttttttt 1380
 ttatgtttccctt gggatgttccatgg tttttttttt cttttttttt cttttttttt 1440
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 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 2460
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 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 2640
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 2700
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 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3180
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3240
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3300
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3360
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3420
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3480
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3540
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3600
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3660
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3720
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3780
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3840
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3900
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 3960
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 4020
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 4080
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 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 4200
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 4260
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 4320
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 4380
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 4440
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 4500
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 4560
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 4620
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 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 4740
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 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 4860
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 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 5160
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 5220
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 5280
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 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 5460
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 5520
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 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 5820
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 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 5940
 atttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 6000

(2) INFORMATION ON SEQ ID NO. 4:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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gccacatssc cgggggttttgc gggcccccgc gatgttttcc agagctttc aagtgggaag 60
aggagagcga caacgtgaaa atgccccgtg cggggcgctc caccggagtc ctgcccagctg120
tcccgccgttg gggtgacgt ctgattttatc aagctccccca tccaccatatac tgagttactg180
actttctcagg actgacacct acagcatcg gtacacacgt ttcccttagca tgacttgcgt240
ctgatcagca aacaagaaaa ttgtctccc gtatgtctgg ggcgtgttca ccacctacaa300
ccacagagct gtcatggctg ccatctctac ttccatccct gtaatttcac agccccagtt360
cacagccatg aatgaaccac agtgcttcta caacgagttcc attgccttct t 411

```

(2) INFORMATION ON SEQ ID NO. 6:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3181 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

cgggtggggg gggagcaggg gggacacgtg ccccgaaac ccgggtgggc acacacacgc 60
 actgcgcctg tcagttagtgg acatgttaat ccagtcgggt ttttcttgc gcattccgc 120
 tcccttcctt ccatagccac gtcacaaacc ccaggatggc catggccggg taaaagcaagg 180
 gccattttaga tttagaagggt ttttaagatc cgcataatgtgg agcagcagcc actgcacagg 240
 aggagggtgac aaaccatttc caacagcaac acagccacta aaacacaaaaa agggggatttg 300
 ggcggaaaatg gagagccaggc agcaaaaaact acattttgc acattgttggt gtcggatctat 360
 tggctgtatct atgccttca actagaaaaat tctaattgtt ggcataatgttca gttttttca 420
 ggtccagatg agtttttttc tgctgtttt aatgtggaaac agactcatac cacacttaca 480
 attaaaggta agccccagaa gtgataatgtt caggggaggaa aagtgcgaatg cattatgtta 540
 atagtgcacg caaaggggacc agggggagggy cattgcctt ttttcccaac gttt 500
 gtgtatgttct ttgaaatcttca atcaggatgtt ctcagatgtcc cccaaatgttcc gtttccatgt 660
 agccccgggc atgtatgtat ccccaagaca ttttttttttgc ctttttttttgc ctgccttttgc 720
 gtcagaaaaa ggaaccacaa gtgagcttgc gagagacggc gattttccggg ctgagaagggc 780
 agtagtttttcc aaaaacacata gtttttttttgc aaaaacatgtt aaaaatattt agaactgc 840
 agcaaatttgc tagtcagggtt gaaatgttca attttttttttgc gtttttttttgc 900
 atgtttttttcc cttttccatc ttttttttttgc gtttttttttgc 960
 gtttttttttgc aacttccatc gtttttttttgc 1020
 gtccgaggct gtttttttttgc 1080
 tccctgttag ttttttttttgc 1140
 taacaccccc tagcaaaact cacagactt ttttttttttgc 1200
 ttcccttttgc ctttgcatttttgc 1260
 gcaattttttgc catatatttttgc 1320
 ccccatccatc ccaatccatc 1380
 ccaatccatc 1440
 gagatacttc ccaaaatccatc 1500
 caacttttcc cttttttttgc 1560
 ttttttttttgc 1620
 cccatccatc 1680
 atgttttttgc 1740
 ctctcacatgtt tagtgcatttgc 1800
 ttttttttttgc 1860
 gtttttttttgc 1920
 agcaatgttgc ttttttttttgc 1980
 gtgttttttgc 2040
 cggcagatgc ttttttttttgc 2100
 agagcagggtt atgttttttgc 2160
 ctttttttttgc 2220
 ttttttttttgc 2280
 catagatgc ttttttttttgc 2340
 ggcacacagtttgc ttttttttttgc 2400
 atgttttttgc 2460
 ctttttttttgc 2520
 agtcccttgc gtttttttttgc 2580
 tagaaatgttgc ttttttttttgc 2640
 aacacttttgc ttttttttttgc 2700
 ctttttttttgc 2760
 atcttttttgc ttttttttttgc 2820
 ggaqgttgc ttttttttttgc 2880
 tggccgttgc gtttttttttgc 2940
 tagtttttttgc ttttttttttgc 3000

ctgtgaaat gtttttttttgc 3060
 atgttttttgc 3120
 ttttttttttgc 3180
 a

(2) INFORMATION ON SEQ ID NO. 7:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1964 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

(2) INFORMATION ON SEQ ID NO. 8:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1702 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ggacacccca ggtatgtgga cgagcagttc ctgtcacgcc tcttccatt tggggccctg 60
 gtgatcatgt tctggctct gatggctaa tgctggctc ctgcgtacat ccgtggcagg 120
 gctctggact ggtagcgtc caccggcaat ctgttggttt ggcttcctgg ctaatcttga 180
 ctcttggat cagtggatc agtaaacat caaggatgt tggtttctca tcagagcttt 240
 ggaactcgag accagttggc gatgaccctt gaatacgcc accgtgtaa acacttata 300
 acttcaggcc ttggcattgt gtcatctc atgggtgca ccatgaaatc ttgtttcagc 360
 cagttctgca ggttctgact ctgcagaggaa aagaggcaga aagagagaaa ctgtcagatg 420
 ataatttcac ctgagtttaa tattacagaa acaaaggat gcaccaaata gttttctgg 480
 aaatttcac gtctttaaat accccttggt aagtgtctt tgaaggcagt ggggggtctt 540
 catagataga gtttccccctt tcaaatccca gtgcgcgtttt gttttcttc ttccccctcc 600
 cacttcccccctt ctgttccctc tgtagatggat caaaggaaattt ctgtccccata aaaatcataa 660
 ttgcagttagc taaaatgggg gtcacttcgtt gaaatccca gagactcaaa gatcttttat 720
 ttgcctctggg ctgtgtcttgc tgcttttgc ctcagagaaac aacttggatg atttcttgg 780
 ttctctggcat aaattttttcc ttgtggataca tggtggcttaa ctccacagggt tcccatcagc 840
 ttcttccttaa aaactatgtt catcttcctc ttcttcggcc agacatataa gcccagaata 900
 ctggcgaagc tgagactgac tactgtgcat taggaagac ctggagttagc gactttgggt 960
 ggttttggag ctccggggca gtaataactt aacaaggcago ctgttccctt aggctgcagai120
 agcttgaatg catcttcctcc cagaacctgc cacaggaaac tgggggctttt gtcaaggcag1080
 cccaaactggca tggaaaaaaac caccatctc agaaggcagat ttgttcttta tgaaggaggc1140
 agggaaagggg aaacccacat gtgaccctgtg ttttggatgg gcttggataga gttccctgtaa1200
 aactcttgtt atgtgtgtcta aaaccaggaa aycatgtgac tggcaaggag gcaaccctgt1260
 atgatttgtta aagccagggtg gcaaggccctt ggggagcccc agcacaatga tattgtgtgg1320
 ttctccctcc ttgtggaaatcg agggaaattt atctttccca ataccttggat ttgtatttca1380
 gtttcataag ctcttccttc tgaaatgtt tgaggggacta tggatccaaag caggtaggc1440
 tggcacctg tgggaaacatgt ttttgcgtctg ctcttcggcc ttcatccccag aaatccagcc1500
 ttcttggaa gaccccaaaatggaggag atggggcttcc ctcttggccct ctcttcatac1560

tggccatcc acactgtcc tggcttaacc cagaagaac caacaaatgg gtagggaaagc1620
 cccatctaat tgggtttttt ttttcaatta tggacggcata ttgttttggt tggaaacaaa1680
 agtttttggaa gggggatgtt gg 1702

(2) INFORMATION ON SEQ ID NO. 9:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2067 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

(2) INFORMATION ON SEQ ID NO. 12:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2548 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ggcccgagcc	tcatctgcca	ccgcgtctg	gttggagctg	tttgtcttgta	tgctcagcga	60
ggccggggaa	gaccggggag	agagatggc	cggatccccc	gccccgatgt	gtgcggccgg	120
cccggttac	gcacaaagcc	ggccatcccc	ggctctgggt	ggccggatgt	accacggccc	180
gggagcagcc	cgcgagacgc	cacggtgccc	ctatggccc	cgccggccca	cgccggccgg	240
cgggagcaggc	gaaggcgcgc	gagagaaacgc	gccccgggg	ggccgggggt	cagtcagcga	300
cccttcgtcc	actcgccgc	agccggaggt	gacgttgtag	cgccggacgg	ggggccaggg	360
agggttcgc	ggggcccccc	ctgtgtcccc	ggccggccc	tcatggccgc	catccgcaag	420
aagtgttgg	tgttggcga	cgccgtgtgt	ggcaacagct	gctgtgtat	ctgtgtca	480
aaggacgagt	ccccccgggt	tgatctggcc	accgttctcg	aaactatgt	ggccgacatgt	540
gagggttggac	gcaaaacgggt	ggagggtggcg	ctgtgggaca	cgggggccca	gggaggatac	600
gaccggctgc	ggccgtctcc	ctacccggac	accggactca	ttccatgttg	cttcgttgcgt	660
gacagccccg	actcgcttgc	gaaatcccc	gaaatgggg	ggggactctt	ggggactctt	720
tgttcccaat	tgcggccat	ctgtgtggcc	aaaaaaaaag	acccgtcgac	gacgagcatg	780
tgcgcacaga	gtggccggcc	atggaaaggc	acccgtcg	ggccggccca	ggccggccca	840
tggccgttgc	catccaaaggc	tacgactacc	tcgatgtgtc	tgcgaagacc	aaggaaaggc	900
tgccggggat	cttggaaaggc	ggccacggcc	ccggcgctca	gaaaggctac	ggctcccaaga	960
acggctgtca	caactgttgc	aaatgttctat	ggggccggcg	ccgtcgccgc	ctggccgttgc	1020
cgggacacgg	ccccctccgt	gaccagttcc	ccggqagccc	ggggaggggg	agaccgggtt	1080
ccccacaaagg	ccccacggcc	ctgcgttggcc	ttgtgtgtgt	gacggcttgg	gttgcggccal	1140
ggacttggcc	ttggccacggg	ggccccccat	ccaggatgtt	gtgtgtgtcc	agttgtgttc	1200
cacaggctcc	ggttcccccc	tgatgtccaa	gggtccccctg	agatgttttt	tcttgaaggatc	1260
cggggttctcg	agggttgttgc	ttgtgttgcgt	tttgcgttcc	ttccggccat	tttccacccal	1320
ccccccgtcc	ttatccccggg	ggggggattt	ggccggggag	ttttttccgg	ccccatcagal	1380
tgttgcgtcc	taaccacggg	gagcttggata	ttcccttgcgt	gttatatatat	tttttttttttt	1440
ttgggggggg	gggggttgg	ggggggatgtt	atataatat	atataatattt	tttttttttttt	1500
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ggctggggcca gactccgcg caagcatgaa caggacttga ccatctttcc aaccctggg1620
 gaagacattt gcaactgact tggggaggac acagcttcag cacagccctt cctgcggggcc1680
 agcccgctgc gaaccttcca ccagctaccc gagggagggag ggaggatgcg ctgtgggggt1740
 gtttttgcca taagcgaact ttgtgcctgt cctagaatgtg aaatttgttc agtccaaagaal800
 actgtatgtta ttgtatgttataaaggcata aaatttgtttt ttttatctt tgacaatgt1860
 ttccatgtt tgacactta tgcaactcgtc atttgcatac gacagttagca ttctgaccac1920
 acttgtacgc tgtaaccccta tctactttcg atgtttttaa aaaaatgactt ttacaacggal980
 gaggaaaaag aaacccacta aattttgtt tgtttccctt aagaatgtgg caaacactgtt2040
 ttgtgatttt atttgtgcag gtcatgcaca cagttttgtat aaaggccagt aacaagtatt2100
 gggccctat tttttttttt tccacaaggc attctctaaat gctatgtgaa attttctctg2160
 cacccctgtt cagagaatac acctggccccc gtatatctt tttttccctt cccctcccttcc2220
 cagttgtact tctactaaat tggttctt tttttttttttt tttaaataaa ctgacaaatg2280
 acaaaaatgtt gagctttatgtt tgttttttttt aaaggcttcat aagctgtgtt tacagttttt2340
 tatgtaaaaat attaaaaagac tatgtatgtat acatttttttt aaaaagaatc ttgtggttt2400
 atatgtgttca aaaataccct tggtaatttgg gacaaggaa gatattctcc taggcgagat2460
 ccttttttgc caactccgtt tccccatataat ccaaattgtatg aatgtggat gaaatccctt2520
 tgagacatc tgggggttgg gtgaccaa 2548

EXCLUDED FROM PUBLIC RELEASE

(2) INFORMATION ON SEQ ID NO. 13:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1673 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vi) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

(2) INFORMATION ON SEQ ID NO. 14:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1593 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ggggcccgagg	cgcgcggccgg	cgcggaggtgg	ctggcccttgcg	cggggacact	cagagcccg	60
tggggggggg	gaaggggcgca	tgccccccacag	ggttatgcctc	cggggccgggg	cggccctgggg	120
cttcaggatc	tcaggggggca	tagactttcac	cacgggttttgc	tgcatcacc	ggattacacc	180
aggaaagcaag	gcccggactgc	caactctgtt	cctggagatgt	tcatcttgcg	tattgacggc	240
ttttggggacag	agtccatgc	tcatctgtat	gcccggacaca	ggattaaaacg	acggacgtcc	300
cacgttgttc	tccaaaaata	caggggggaaat	acttacttata	gttcccccaca	atgtatctaa	360
gatggggaaag	cccatccctt	caaataatccaa	ttagaatctcg	aaccacaggaa	atccaaaccc	420
atttgttaccc	cgcacaaacag	aaaggggcccg	cctttttgttgc	cagtcgtca	cattgtatgc	480
aaaagacagg	tagtggggc	ttccctataac	tcggccaaat	ggctcttatto	aaactagcaat	540
atacaagatg	cggtttccacgg	acatgtcgccg	gttttcatttc	ctatgttcacc	tcaaaacccgg	600
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gggtttttatgt	acccgtccggc	tggaaggccgg	atgttgttgc	ttccgggttgc	aaaggatcc	780
ggccgggttcag	ggggggggcaca	ggaggatccgg	ctctgttgcaca	aatgttgggg	tggcatatgt	840
ggtgtgttgg	ttaaggccgcg	ggataagttac	cggtttccat	atgttgttgcgt	ttgttgcgcac	900
tgcacccatca	accccttcaagc	aaagggttccat	ttttttccat	aaaggggggat	gtactgtccaa	960
accacccggaa	gagccccccac	aaaggccccca	gggggttgc	acacggttcac	ttctgtatcc1020	1080
aaagcttaag	tctctgcagg	cgtggccacgc	acggccgcac	ccaccccaacg	gcacttacac1080	1140
gagaagacat	tcatgttttt	ggggcagaaagg	atttgttcgc	tttgttcaactc	caaatctaata1140	1200
tttcggatcc	tagacccctta	ttccatgtttt	tatgttggaa	aaaggatctgg	aggcaatgtc1200	1260
ctgttatgt	aaaaaaaaat	acatctttgt	atgtttttgc	actcttttttgc	gggtctgcaal1260	
taatgtat	taaaggcaaa	atttttttgt	tgtcatactc	cacaattttac	atgtatattal320	
caggccatcaa	acacataaaac	atcaagatgt	tttggaaactgt	ctttagttgt	ttccctggacal380	
atgttgtttt	ggaaatgttgg	ttaaaatggaa	ataaaactatgt	tgtttttttca	catataatgc1440	
tttgtttttt	atgtgtttta	acttattacag	tgcatgttgc	ggagaaatcc	cctgaaatttc1500	
atgttttttt	tatcccaaaa	attatgtccac	tgcgtgcacaa	aaacacataata	aatacataaa1560	
atgttttttt	aaaaaaaaaa	aaaaaaaaaa	aaa			193

(2) INFORMATION ON SEQ ID NO. 17:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1722 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

cattgtttgc	caaataccta	ggcagcatgg	acccatgtt	tctctgggta	cttctgcccc	60
tagtcacat	ggccatgggg	cagtatggc	attatggata	ccatcacccg	cagatctatcg	120
actacagoga	tgatgggtgg	tgaaatttga	acccggcaagg	cttcacgtac	catgttcccc	180
aggggcagggt	gatagtggcc	gtgaggagca	tcttcacggaa	gaaggaaatgt	tttgtcagaca	240
aatggaaacta	ccgcgttcatg	cccacaccac	agagcctcg	ggaaccacacg	gagtgtctgt	300
ggggaggagat	caaacgggtc	ggcatggaat	tgatccacag	tgctccaaac	aatgggtctgg	360
tggcaggatt	ccacggccgc	tacttcgtat	cagtgttgg	tcggggaaatgg	cattttactt	420
ttgttcgtcata	cagaacaggg	tgcccatattt	cttcgggtgt	aaacaacaaag	ttatccaggtc	480
actatgggtga	ggaatatggac	atgatttttct	acaatttatga	ttactatatc	cgagggacaa	540
caaccaactt	cttcgttcgtg	gaaagggtac	gccatgtggaa	gttcataatgt	ttccggatgtga	600
ctgtaaatcga	ctgtgttattt	gcaatgtttt	atgtttggca	cataccaaaat	ctgggttggaa	660
ggaaaggggc	cgggggacagg	agggttttcca	catatgtttaa	catcagtgtt	atccctttatca	720
gaagttttcgt	ctgtttttttt	tcctttttttcc	ttgtgttggta	actgttcgtt	caacttcgtt	780
ggcccttttcgt	actatgttca	cactttttat	aaaatccaca	ataaaaatcat	gttttcactt	840
ttttccatctgt	ttcatatggaa	ctgtttttata	ttgtatgtat	tggtttccctt	gcacacccaca	900
tatacatgtc	gcgtatcttac	acggccggctt	ctggagocacc	atgttcgcac	ttgttcactgtc	960
tttttacttgc	agaatgttac	gcaatgttca	catatgtggag	gggagggacca	gaacttggagg	1020
agagggttcac	ttggatgttcc	ctacatgttca	gtctgttttt	atgtatgtca	gtttcccccac	1080
caaaaaggcagg	ctttttgtccc	tgaggacat	ctttcccaact	ccctgttccca	catggccatc	1140
gcatgttttag	caatccaaatg	gcaagatgtt	ttgttccttgg	agtgttggaga	ctggggaaatgt	1200
aaatggggaa	atggaaagggt	ttggggccat	agctgttttttt	agggtttggaa	ggattttcgtt	1260
aatttagaaaga	caaaatgttag	cataccatgtt	aaaaggaaatgt	agtgttggggg	ccaggggaaac	1320
ccgttggatgtt	Cacttttttttt	tgatggataaa	aaaaaaatgg	agtgttggggg	catggaaatgt	1380
ggatccatgtt	ttggaaactttt	ttggggatgtt	aaatggggaa	catggaaatgt	tttttttttttt	1440
			agtgttgggg	tttttttttttt	aaatggggaa	1440

(2) INFORMATION ON SEQ ID NO. 18:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1648 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (viii) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

tgaccaagaa	acaggggccta	aggatcattt	ttcggatgc	atcacggctc	atccccggc	60
tcgttccctc	cagtgggtgg	cgggccaccc	tcgacactgt	acgcagagag	ctacggaggg	120
catggccacgg	ggccatggaca	ggacccacag	ggactgtga	ggccctctat	acgcacccgtca	240
ctgaaaaatat	cccagattca	tgagagaact	ggccggaggg	gaccctactgt	catcacctgt	240
atagggaaaa	gatcattcac	caggggccaa	gagatgtc	acggccggat	gtttccatgt	300
tgcccttttgt	tcacccgttc	tgccgttta	tgacttttga	aaaaacaaaag	atatttttgt	360
tttggggat	agagggtggg	tgggggaaaa	aaaaaaaaatc	atbtggttt	gttttttgtcc	420
tatccctcca	aatgcagcag	ggcccttttagt	ttctgtttaa	agctgcacta	taatttttgta	480
tctacattt	atcacaaaaa	ggaaacctccc	cttttgacaa	caactgggt	aggcagctgt	540
taatccaaac	atttgtccat	cacttggcc	aagtggaaaa	atgtttcaaa	atccaaagag	600
aaacatgtgc	cagaatgtaa	ctgaccctta	ttccggatgt	ccctccggca	ggcagaaggaa	660
gacatccca	gcatggggaa	gggttttatet	tttccatctca	ggtcagggt	acaatggggg	720
aaggttttat	ttatagaacte	ccaaacggccc	acccatctcc	ttccggccaccc	ccatggccgc	780
tgccctcccc	atcccccattcc	caacatccct	tttccatcttc	ttccatccat	ttccatccat	840
ttgttacaat	caacaatgtt	cacttcccaat	aaaatatatac	aatagggttt	ttccctcttt	900
atttttttaa	tagttatttt	ttatgttatta	atgtggatac	tttccatccat	ttccatccat	960
tcagtgtta	agttggggaa	aagtttttttgc	tttccatccat	ttccatccat	ttccatccat	1020
ttggggggat	cttcccttgc	ttatccatccat	ttatgttgc	ttatgttgc	ttatgttgc	1080
tcttggaaag	ggaaaaaaagac	caccatgttc	ttatgttgc	ttatgttgc	ttatgttgc	1140
tatcttaatg	cacttgttttgc	gacacatttc	ttatgttgc	ttatgttgc	ttatgttgc	1140
aggatggaaat	gtcttttttttt	tagggaaatgt	ttatgttgc	ttatgttgc	ttatgttgc	1200
gtacatgtat	ggggccatgtt	ttggggggaa	ttatgttgc	ttatgttgc	ttatgttgc	1260
tcacagctgg	cttttccctcac	ttggggaaaag	ttatgttgc	ttatgttgc	ttatgttgc	1320
ctcggccagg	acaccggccat	ctggggaccc	ttatgttgc	ttatgttgc	ttatgttgc	1380
gcacatgtcc	tcacccgttc	atttggggaa	ttatgttgc	ttatgttgc	ttatgttgc	1440
tgccgttatttgc	ctgtgttgcac	gttttttttttt	ttatgttgc	ttatgttgc	ttatgttgc	1500
ttttccatgttgc	tttttttttttt	tttttttttttt	ttatgttgc	ttatgttgc	ttatgttgc	1560

aagaatcc taattcaac cttaaaaa

1648

(2) INFORMATION ON SEQ ID NO. 20:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1610 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

gcccgcgtat tggacgcgtg gggcgaggcg gaggagagcc gtgcgcacgg cgtatgtggg 60
 gcccgtgtcga gaccgcgcgtg tggcgcaaggc aaggacccctt aaaataaaaca gcctcttacct 120
 tgcgacgcgtt ctcccccaagg cttgcgttcgg agtgcgtccggc gctgcggggcc cgctccgacg 180
 cggaaagatct gactgcggcc atgagcggca atgagtgtt caagtgttgaa cgatctggcc 240
 actggggcccg ggaatgtccat actgggtggag gcccgtggccgt tggaaatgaga agccgtggca 300
 gaggttttccca gtttggtttcc tcgttcttc catagatttt ttatcgctgt ggttagtgtt 360
 gtcatcttgc caaggatgtt gatcttcagg aggtgcgtt ctataactgc ggttagaggtt 420
 gccacatttgc caaggacttcg aaggagccca agagagagcc agagaatgc tgctacaatc 480
 gtggcaaaaagg aggccatctg gtcgtgtact ggccatccatc agatgtggcggc aatgtctatt 540
 ctttgtggaga attccggacac attcaaaaaag actgcaccaaa agtgaatgtc tatagggtgtt 600
 gtgaaatcttgc ttcatgtggcc atcaacttgc caaagaccaaa tgaatgtcaac tgtttacccgct 660
 gtggcgagtc agggcacccctt gcacacggat gcaacatggta ggctacacggc taattttttt 720
 cttttgtcgc ccctccctttt tctgttggat gttgttattttttttctgttca atcccttttca 780
 ctggccaaagg gttttggcaga; agggccaaact cccaggcccg tgagcttttac ttgcgtgtca 840
 aaaaaaaaaagggtggaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 gtttagtttgc tgtaggggtt: tatgttataat gttttgtttaa agaacccccc ttccgtggcca 960
 ctgggtgaata gggattgtat aatgggaaga gttgagttcag accgttaaagg ccgtccctgggg1020
 ttcccttgcac atgtttccat tgtagggat aaaaaatttc tggaaatgttca tatqaacttc1080
 cataaaataac tttaatatttgc ttaataatgtat gttcttggat tgctgtaccc cagtagcttat1140
 taaaataacat caaataacat: ctgttgcagg ccctacatag aacatacagtt tgagtgggg1200
 taacaaaaaa gataaaacatc cgtgttgcagg gttgttgcagg agaaatcgaa ataaaaggct1260
 aaaaaaaaaa gataaaacatc cgtgttgcagg gttgttgcagg agaaatcgaa ataaaaggct1320
 tttagacacaa ttattttcaaa agactaaatc taaaaccccaag agtaaaacatc aatgtcagaa1380
 gtttagcataa ttggagatc ttccaggatc gcagagaaat gcattttcac agaaatcaag1440
 atgtttagatcataatc atcaacttaga caactgtgtt ccattttgttgc taatcgttgc1500
 taaaatgtca gatggaaaga gcaactgttgc ttcttagaaaa tagaaaaatgttca atttttaaact1560
 attccaataa agctggagga ggaaggggaa aaaaaaaaaa aaaaaaaaaa 1610

(2) INFORMATION ON SEQ ID NO. 21:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1108 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ggaggcgcgg ggagagtagg gtgctgttgt ctgagctaga gggatgaagct ggcggacagg 60
 aggatggcgc tatgcagggt atagactaga gaacaagacc tctgtctccg tagcatctcg 120
 ggcgagcagt ctgaatggcca gaatggataa ccgttttgc acagcatttg taattgtctg 180
 tggctttagc ctcattttca ccatctacat ggccgcctcc attggcacag acttctgtta 240
 tgaatatcg agtccatcg aagaaaaatc cagtgttgc aataaaaagca tctggatgtga 300
 attcattatgt gatggggcgc atggaaagac ttataatgtat gcactttttc gataacaatgg 360
 cacagtggg tttgtggagac ggtgtatcac catacccaaa aacatgcattt ggtatagccc 420
 accggaaagg acagactat ttgatgttgtt cacaaaaatgt gtgatgtttca cactaactgt 480
 gcagttccatg gagaaatttg ttgatcccg aaaccacaaat agccggatgtt atctcccttag 540
 gacattatctt tggcggttgc agttccctt accttttgtg agtttagtt tgatgtgtt 600
 tggggcttgc atcggaacctt gtgtttgcattt ttgcggaaac ttatataccca ccattgcac 660
 gggcatttcc catctccctt caggcttgc tacactggc tcqatgttgc ttatgttgc 720
 tggaaatggaa ctactccacc agaaaactaga gctccctgac aatgtatccg gtgaaatttgg 780
 atggcccttc tggctcggtt gtgttcttcg tcccttacag ttcatggcattt ctgtctctttt 840
 catctgggtt gtcacacca accggaaaga gtacacccat atgaaaggcat atcggtggc 900
 atgagcaaga aactgcctgc ttacaatttgc ccattttttt tttttttaaa taatactgtat 960
 attttccca cctctcaattt gtttttaattt ttaaattttgg ggatataccca ttttattatgt1020
 gaaaatccat ttaattttata caccatttcac cactaaatac ccccccttaat accccctaaal1080
 atttaagggg gtttacccat aagcgatg 1108

(2) INFORMATION ON SEQ ID NO. 22:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 675 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
- (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
- (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

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agggaaagag agagagaggc cttagcgaac acaatcacat gttttcttgc ttgttcc 60
cgggatgggg ctgtttttggg gtttggact ctgaaccoga gcgggggttcc ttgcgttgac120
tttgcattcg gtccctaaat qccttcctcc actccctcc cttgggttca ggggcaca240
ggccctctct cagagcacgg gcagcacccgt ctccgttggacc ccttgttgcc agcccttgca240
gacgacgtcg gtggggaggga qcatgattt ggagggtggq aagtcaactcc ttgttccctgg300
aggggggtggg ctgtgtgcct agtcaagtgt gactccggg ttgggtgggg cgacacagg360
tctggggctt ccataccctt ctgtttaaat tcacacgaga tagtccaggg ctttcacgcg420
cccacgttgg atgataatcc tctgttccccca cactctaagg cctcccttgag atttutttgg480
ggtttacacc acgttttttttgc ttgttccagg ttgttacagga gatgtggtc ctgtccctct540
ccctgggtccc tagggggccctt ccctgttagct ttatgttacc ccatgtgggt600
gggttggggg tctgtgcggg tgctcaggta agttttggggg ctcccaaggaa gcggtcccca660
agaacgggggg gggag 675

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(2) INFORMATION ON SEQ ID NO. 23:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 350 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

agcagagcaa ggttgggttc gtcctctgg cagaacctcg gctctcagga ggtccttgg 60
 ccaggaaaca gctgottctc tggggctgg gggttctaacc ttccctggca gcccctggc120
 actaaaccac ctggaaaccg gggaaaccaa cggcctggag tgccaaaccc ttctgtgtcta180
 tttttccac aaaaacgggg gcaatggctc ttgaggagcc catttggaa gaactgggc240

ctctaatggg gcaaatggat tctgcagggg gctgcagttt ggcagggaaa attccttcaa300
 acaagggtt ccacccaaac ccaggccccg gcttcaaatg gccagaaaaa 350

(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 746 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ccccccctcc tccggctttt tttttttat ttaagaaaaat ttatttctac ttctacagca 60
 gaaatacgcgaa atatgtacag gtgtggcaa atcatactt atgaaatggaa tcctcatacc120
 acatcccttt taatacaggc acgttataac atataatccctg gattttc当地 atccagccaa180
 cacggatacc tctgtactc tggtttggcc ttcatagctg ctccctctt cagacgagct240
 ttcttttcta agtgcacgt tggttaaagtgc tctgtgtttt gggcagcctt ctggccctca300
 ataaccatgaa agatgcatacc taccaacgcg aggccaatca tttagatagct gatcttcaact360
 cgcatcttgtt ctcttgccgc atcaacgcata tccaacgaga cagtctctgg gatttcatct420
 tccttttgcgaa agcgacatgaa ccataatgggg atctttttt gccaatatccgtt aggtttgtgt480
 aaaggcactc tggtgttaaagt gcggtgtggaa gtcctcggtt ttttgc当地 540
 aatccattta ttctcttcaa atcagagctt ctggtaagcc tttagagatga gaaaacatct600
 ctttcacata accttacaca gcttcctgtt gccaggcgc当地 gaccgcgtgag gctccccatg660
 gccacttgctt acttcggccgc当地 ccacgc当地 acttcggccgg ggacgggtggc gctgtgtgagc720
 tcaatgtcac ccagcggtgg agtggg 746

(2) INFORMATION ON SEQ ID NO. 25:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 217 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

agtgttatggc agcaaatggg ggatcataac ttcagtttta ttgtatgatta ttcatctca 60
 gatggaggag ttatccgtc agccacttca gtttgc当地 aaaacaggag cccacaggac120
 ccaaggaaactttaaaggagg accaggaaacc taggtttttt ctttcaaaaa attggccctca180
 gccc当地aaa tgaaggaaaa aatttagggac ctttttt 217

(2) INFORMATION ON SEQ ID NO. 26:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 392 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

gcggatccgg cgttctccac tgatctttc caaggctgt a gagatggc ggcggcttt 60
 cggaggccg ctaagtccccg gcagcggaa cacagagac gaaacgtga ctaccgtaaa 120
 aaacaagaat acctcaaaacg tttccggaa aaggctttt aaaaaaatcc agatgaattc 180
 tactacaaa tgactcgggt taaactcccg ggtggatgtc attattataa ggagacttaag 240
 gaagaatcaa cccagagaca actaaactgt atgagactt caggacgtca aatataatagg 300
 aagggaagag ggtgcagaag ctaagaaat cgaagactaa aatcagggcc catctgcggg 360
 ttgcaggaga ggcaggaaaa ggtttttt tt 392

(2) INFORMATION ON SEQ ID NO. 27:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1796 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

(2) INFORMATION ON SEQ ID NO. 29:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2927 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

(2) INFORMATION ON SEQ ID NO. 30:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 743 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

tccgtggggc tttaaaaaaat ggttgtgggt gtgtggggtt ttttgaggtg ggagaggatg 60
 tggaaaatc ttttcaggg aaatgggtt cgtgcagagg taaggatgtg ttctgtatc120
 gatccgcaga cacccagaag gggggcgc actgcgtgc tgggggtgcc aaggattcg180
 agacctccaa catactgtc tgaactgtc ggcgtggcc atggccccc tcgccaaggct240
 ggttggatg cccctggjc tttagtgcac aaggtcttag ctcaagaaca cagcagccccc300
 atcttcgtt ttcagggtt gtgtatggg ccaaggaaaa acattttatc ttactattt360
 accttaatc aaatgggtt tagtgcgttgcgcacca ccctttttat cacttttaaa420
 ttgcactt atttttttc ttccatgtc gtctctggc cattttggga tttgtatgtt480
 agagctgtg agagaggagt caggcgcgt tccccccat ggtccgtggcc tccacactgccc540
 ctctttcc tgccttcc cccgtttcca atttgcctt cagagaactt aagtcaaggaa600
 gatgttataat tcaacggccca gggcacatc ttatattatc tttttatgtt ggccaaacaga660
 acttgattgt aaataataat aaagaatct gttatataact tttcaaaaatc caaaaaaaaaag720
 taggggggt aaaaaaaaaagg gcg 743

(2) INFORMATION ON SEQ ID NO. 31:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1667 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vi) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

(2) INFORMATION ON SEQ ID NO. 32:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

cgtggtaggc acttcatca gtttactga ttgaaacat tggtgactgt ggcttctatc 60
agagtgtcta cctttacag ctctgaccct acctcatatc atttgctgt ttaatctac120
gggggctgag aatttgtgaa accagtgtt tgagaatgt atataatctg aatcaataag180
ctctgaatgg gggacaaagaa acgtcttat agcacaaaaga tgcatggact tcatgacago240
tcttttgtt 249

```

(2) INFORMATION ON SEQ ID NO. 33:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1246 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

(2) INFORMATION ON SEQ ID NO. 34:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 215 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```

gggaaggcatt ttggatatga tgcaggaaat ctcttcctgg agtcaaaaat tcccaagagg 60
tgctgttattt ttaagaataatg gagttttttt aaataaatatg taagcttgc cccatgttgg 120
ccggcacaat tttttcaatg gtgtttttt gaagaatgtt tttcatctgg tcaattttaa 180
gaaaaataaac tagaaatgg aqagqqqqqq aqaga 215

```

(2) INFORMATION ON SEQ ID NO. 35:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 734 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

gctgccgggg gcctggggct cggcgtcggt ccccgaaaaa tggggagagg tggcagcatg 60
 tcggccgagc tgggactcggt gtgcatttggggcgtgtga acgacggcgttgcagcaggct120
 gtggccgggc ggccggggta ttcccaagcc atccagcccc ggctagtggc ggtcagcaal180
 accaaacactg cagacatgtt gatcgaggcc tatggacatggcagcgcac ttttggcgag240
 aactacgttc agaaactgtt cggaaaactca taaaatccccaaattctgtc ttgtgtct300
 gagataacaatggcactt tgccacttca cagaacaaatgtcaacaa attgtggct360
 gtcccaatcttccatgttggaaactgtt gattctgtga agttggcaga caaatgtgaaac420
 agttcttggc agagaaagg ttcttcttggaa aggttaaagg ttatrgtcca gattaacacc480
 agccggaaag agatgttcaaa tggcttccatcccttccaga ccatagccat cgtggagcac540
 ataaacgcctt aatgttccatggatgtt ttccatgttgcatggatgttgcatgg600
 catgatcttca tcaaggacc aaatccagac ttccatgttgcatggatgttgcatgg660
 actgtgttggaa aatgttgcac atccctgttgc aacagggttgcatgttgcatgg720
 tctgttggatgttgcatggatgttgcatggatgttgcatggatgttgcatgg780
 734

(2) INFORMATION ON SEQ ID NO. 36:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

gctgctgggg agccactgaa ccaacccggag acccgctggt cccacgtgaa gcagctgtcc 60
tggtgtggag gtacagacgt agaccaggac tggtcctcc agccccctgg tagcctctgc120
tgcaactgaa ctggcagctt ttgcccgtgc ctttagtctt qcatgtatgc gcccgtgaagg180
ttctgcctct ctgttttggaa atcccttc cctccatgtt tttggggacc tgcaagggtg240
tgaggcacgt gaggcatcg ccatgcgtat ttacaggcc ttttccttg gactgttcc300
aaaggartga cttt

```

314

(2) INFORMATION ON SEQ ID NO. 37:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1839 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

gcgggcgagg gcggagaaca agagcggccg ggagtaaggc ggagtggagag gaggagcttg 60
 atggaaaggcgt gcgagaaggc ggctaactga tttggaaacc agaggaaagg cgctgttttc 120
 accgaatttag aatcgccgga aaataagaaa gagttttttt gaaggctctcg cgagatcgag 180
 tgagtaacggc tgcccaaggc ggagcgttgc agcaacttcg cggatattga aggagcggcc gaggccagg 300
 ggaggagagg acccgaaatgc ctccatctca agcatcaat gctgaaacgg gcttgatttt 360
 ctctacccgga agccctttc cagaggctgg gacacccgc cacctagcag gaagtcccc 420
 ctcttgcgc tccggccaccc ttcccgaatg tttctgtca cctgtgttag gctccgtccc 480
 cttccgcgc ttataccccc taccqaaaaa ggatacattt agtgctcccc accccagctcc 540
 actaaacggc ctcccgctt cctgtgttg tgccgcgtgt gctgtggggg gggcccccca 600
 cccggggcgt cattcgagcg acctcgccacc acaatgcacg catggacttt gcaagacctt 660
 cagcttgcgtt tggggatcc ttggacccagg agggccctca ggggttccct gtggaggttc 720
 accccagacaa tgccctgcacg cccattggcc caccaccccc agccccggtc aatgggtcag 780
 tccttattgc gctgtttcgta agattcgact gcaactttaa cttcaaggcc ctaaatgccc 840
 agaaaggctgg atatgtggcc gctgtgttgc acaatgtga ttccaaatgaa ttcttgaaaca 900
 tggtgtggaa tagtgaggaa atccagacgcg agatctgtat ccctgttgc ttattttgggg 960
 agagaagctc cgagtacccgt cgtccctctt gttctacga gaaggggcgt cgggtgtttc1020
 tggttccaga caatccatcc ccccttgggtt attacccatc ccctttcaca gggattttgg1080
 gactgtgtgt tttggccatcg ggacgtatgg ttagatctcg ttgtatccag caccggaaac1140
 gggtccacgcg gaatcgactt accaaaaggc aacttgcacca gatttccatca catgactatc1200
 agaaggggaga ccagtatgtat gttctgtggca ttggcttgcg tgaatatggat gatggggacal260
 agctcgccgtt actcccccgtt gtcatgtatcc accacaggcc ctgcgtggac ccctggctcal320
 ctcaagcccg gaagacdtgc cccatttgca agcagccctgt tcatcggtt cctggggaccl380
 aagaccggaa ggaaggaaact caaaggccaaaggagggtga tgaaggggag ccaaggggacc1440
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1839

(2) INFORMATION ON SEQ ID NO. 38:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1931 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

caccggccgc ccatccccctt ttgtgtgttt tggaaaggccg cggagctgtt ggtggctaca 60
 gtttgtgttg gggggcttagg cgaggacgtt tacccggaaatc tggcggggactt gggggctt 120
 ccccatcccg tcacctggaca tgccatccaaatc atcgacgaaa aaaaatgtt aaaaatgtt 180
 ttggaaacgtt agaaggacggc actggcccaatc atcagagagg aaaaagaag aaaaagaagaa 240
 gaaaaggaaaaaaa aaaaagaaaaaaac agacccaaatc aaaaaggatgtt tggccctgtt gggggaaatc 300
 tcatgttccg aaaaaaaaaaaag gagaaatgtt gagatgttccg ttcacaaatgtt gggggctt 360
 ccagaatccc ccattgttccg tccatccatgtt tccatccatgtt cccaaatgtt gggggctt 420
 agtgaaacgtt gaaggccaaatc ctgttggatggatggccgtt gatcttgcggatggccgtt 480
 aaacttggaaatc tggttccatgtt cggccatgtt gatcttgcggatggccgtt 540
 acaaaggaaaaatc ctccatgttccg tccatccatgtt cccaaatgtt gggggctt 600
 gatgttggatggatgttccatgtt cggccatgtt gatcttgcggatggccgtt 660
 gggggaaatqatgatgttccatgtt cccatccatgtt cggccatgtt gatcttgcggatggccgtt 720
 ttgcactctgtt aggaatttttt aagtttttt gaccatcttca aaaaatgtt aaaaatgtt 780
 ctttttgttgcg agatataatcatc ctccatgttgc tataatgttgc gatgttgcggatggccgtt 840
 ggagatgttgcg aacccatgttgc taaaatgttgc aaaaatgttgc gatgttgcggatggccgtt 900
 tcaaaatgttgc ggggttggatggatgttccatgtt cggccatgtt gatcttgcggatggccgtt 960
 gtttccatgtt aacaaatgttgc agatgttccatgtt cggccatgtt gatcttgcggatggccgtt 1020
 tctggaaatatc aaaaaaaaaac tccccccatgttgc gatgttgcggatggccgtt 1080
 tctgcacatgtt ttgcacaaatcatc tccatgttgc gatgttgcggatggccgtt 1140
 atttgttgcgtt gggataacccg tagcaataaaa aaaaatgttgc gatgttgcggatggccgtt 1200
 gcaatgttgcac acacacaccc tttatgttgc gatgttgcggatggccgtt 1260
 aatctgttgcac gatcttgcgtt tttatgttgc gatgttgcggatggccgtt 1320
 catccacaggatc atagcatggatccatgttgc gatgttgcggatggccgtt 1380
 atgttccatgtt ccgttggatccatgttgc gatgttgcggatggccgtt 1440
 tacacagcatgtt gccgcacatgg cggccatgttgc gatgttgcggatggccgtt 1500

 ggaccaatca ctggccatgttgc gatgttgcggatggccgtt 1560
 ttgttgcactt catgttgcgtt ccgttggatccatgttgc gatgttgcggatggccgtt 1620
 ttgttgcactt catgttgcgtt ccgttggatccatgttgc gatgttgcggatggccgtt 1680
 ccacggccgtt ttgttgcgtt ccgttggatccatgttgc gatgttgcggatggccgtt 1740
 gagacacaggatc tccaaatgttgc cggccatgttgc gatgttgcggatggccgtt 1800
 agatgttgcacccatcttggaaatc gggggatgttgc gatgttgcggatggccgtt 1860
 ttttttgcgtt gttttttggatccatgttgc gatgttgcggatggccgtt 1920
 tggccggccacc c
1931

(2) INFORMATION ON SEQ ID NO. 39:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

agttaccatt gccttttctg ttcgtgccg gttttgggtt gctgaaacta gtccaaaaca 60
 ggaatttaa cagacagcca cagccaaaga gtgtcatgtg aattacaaga aatagagccc120
 attttagggaa agatagaact agaaaggcgtt ttcatataa ttccatgttg aacaatttagl80
 tcatacgctt ttatcttgg aagaaggacac aattcaagg ggcaactaagg attttgtaaa240
 acgtgcacataatttac tatggacaa gtgcacat ctctaggaca ttaa 294

(2) INFORMATION ON SEQ ID NO. 40:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 882 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vi) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

882

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 934 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ctcgccggg acacaggag cagcggcac gcgtttcccg caacccgata ccatggaca 60
 ggatttttccc gcttcagccc aacggggagg gcttagttca catagttgcata tagatgaaag120
 agcttattgaa gctttaaaag aattcatgtaa agacggtgca ttggcagttc ttcaacagtt180
 taaaagacagt gatcttcctc atgttcagaa caaaagtgc tttttatgtg gagtcatgaa240
 gacttacagg cagagaaaa aacaaggac caaagttaga gattttatgtg aaggaccaga300
 tgaggcaaaa attaaggcac ttcttggaaag aacaggctac acacttgcata tgaccactgg360
 acagaggaag tatggaggac caccccccaga ttccgtttat tcaggctcagc agccttcgt420
 tggcactgag atatgttgc aagatgtcc aagatgtca tttgaggatg aactttgttc480
 attattttgaa aaggctggac ctatgtggta tttctgtcta atgtatgtc cactcactgg540
 ttccataga gtttatgtcgt ttgttacattt ttgttacaaaa gaagcagtc aggaggctgt600
 taaaactgtat aataatcgat aaatttcgttc tgaaaaacat atttgtgtctt gcatctcagt660
 tgccaacaaat aggctttttg tgggtcttat tcttaaaggta aaaaaccagg aacagatttt720
 tgaagaattt agccaaatggc aagagggtt tacagacgtc atttttatacc accaaaccgg780
 tgcaaaagaaa aaaaacagag gctttttgtt tcttgaatataa gaagatcaca aaacagctgc840
 ccaggcaagg cgttagttaa ttgagttgtt aagtcaaggcttggggggaa tgtttggaaat900
 gtttgaatttgggggtgttcc gctttaggaag gttc 934

SEQUENCE DESCRIPTION

(2) INFORMATION ON SEQ ID NO. 44:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 231 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

ctcgccgg tcaattatgtaa gttccctttat ttattttgtgaa gaaagatttag caagtatgac 60
 gtatgcggaa aatagaatgtt atgttccggc tggtttaaagg ttggggggat atggagatgg120
 atgagggggc gctgtctggg aaggctttgc ttcaacttggaa tttagacttgg gttgcgttgag180
 gaaaataggtt tgtagaatgtaa gaatgggggtt catgacaccc tccataaaaa c 231

(2) INFORMATION ON SEQ ID NO. 46:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 240 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:
- (vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

cgatcacgtt ttcacatgat gctcacgctc agggcgcttc aattatccct ccccacaaaag 60
atagggtggcg cgtgtttcag gggttctgt ctctctctca cagaaaaagaa aaagaaaaaa120
atgtcattag aagaggcgta acacgtcagt ccgtccccag gtttgtgtt ccttgagtggi180
ccgaaagaga tcagttcaa cctgtctgc aggaataaac gcctgcctc ccgacactct240

(2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 228 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:
- (vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

agagcagatc agaggcaggg ggaaaagcac gcagaggagg gagctgaaga gctgagaccc 60
ggagccagg acagttat gaagacaac tgaagggaa actgagatgc tttagaaagcc120
caacctataca actctaccca gaaatacttc ctttagggaa tgtaaaaagt actactggag180
atgaaagacg agaaaaacacg ctatggcag aaggccaagg ggtgataag 228

(2) INFORMATION ON SEQ ID NO. 48:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

aaaaaaaaaa	aaaaaagagt	taatcttagga	gataatgaat	ggcctagtagac	tagataatat	60
atggcccccc	aaggcttgc	cttcgttgc	tggggaaaag	cattttttgtt	accaccaact	120
tgatgtttac	atgtatgttca	atggagaaca	gagaagatcc	ttgttgcaaaa	gggttattaa	180
atatttgtgc	tgtttctgtt	tgagatttgag	aagcttttcc	cacctctcac	ccttattttcc	240
tataaggata	tccaggagaaa	ccaaatcttgc	ctgtggggttt	gggaatgttc	atttccccggg	300
aaaaatgcac	tggatcgatg	actaaatccgt	ggcccttttct	ttttttttttt	tgtaaaggcc	360
attttcaacgc	tggctggcag	tgtgtcgaga	gcctcgaatg	ctctggggcg	tagtgcctt	420
ctgcggccgc	tgacgatgtt	tcggaaaatgt	gagatgttga	gagactttgt	cgaggcaggaa	480
acgggttagt	ggatgtttgg	gcggatgttgg	gaacttttgc	tgatattaca	gtatgttgcgt	540
atcggttaaga	actctgttattt	ggacttgcgt	tttgttgcac	tgtgtgccta	tacctgcctg	600
tgtgtgttgc	atgtgttcggg	ttccattttgtt	tgtatgttgc	ctgtggggaa	cttgcgttgg	660
tcatattttt	tcatttcac	caaaaggcttt	ttttttttttt	ttttttttttt	ttttttttttt	720
caagaacaca	tgaattttttt	ttaacaccag	attatgttgt	taccccaaat	gaacgggtct	780
agccccccttat	ttttttttttt	aggggccata	aggattttttg	ttttttttttt	ttttttttttt	840
ctacttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	900
caatgttgc	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	960
tgtgtgttgc	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	1020
aaaaactgact	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	1080
ctttttgtttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	1140
tacccatgtt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	1200
caggttttcc	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	1220

(2) INFORMATION ON SEQ ID NO. 50:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 231 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

gaggccggga gtggAACccc ctTTTTtag aaggTTGcct gactcagaga cacagaaaacg 60
ggTCCAGGGA tggggAGAGA tggtggAGTA gggAAgggTTT gcatttgcg aaggaaagtTC120
gagaacacac tggggACATTG taacacatTTT gaaCCATCTT ctgtatggaaa ggTTggcc180
ttcaataat qaaqgttcAG qcccaqgtcc tccggcatatG qgaaqadggTC c 231

(2) INFORMATION ON SEQ ID NO. 51:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1340 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

tttggcatca ttatacaattt catagaattt ctgtgaaggc ctttctagtt gagatgttgg 60
 ggttatggg attcttaatgg ttaaccccg aagaaggtaa tttagetttgtt attttatttaa 120
 aaccatcta gctttttactt tatatctggt agaattccag tgatcatctt aataaggat 180
 atttcagaat aattttttttt tccttcagaa taacttggaa tcagatgcta taagggtccc 240
 taggacagt gtgaaatcc cgtaaaagata aatttggatg ttgttaaccaa gtttatattt 300
 aaccaaaggcc ccatttccaa tatgtatattt ttgtttctttt taacttgatgta agtcccttaag 360
 agattacatg cttagggcttg agtcattttatttggatgata atgatggccc acacagtccac 420
 cttaactt ccacatcaagc tagttttccg gctttggcca cggacagtgtt gaccaagata 480
 ttccagatg aaataaaccctt ccacaacccctt ggttaatttttttctttaatccatc 540

 gaagcgaaag cagaaggat cttttcagac tgccctctgt agcctacatt gcagctttcc 600
 aaaacagcgca gctagcactg ggaaaggccca tgggttgacc ccataatttt ctgaggtttt 660
 tttttccat ggtgttaattt tattatcaga aagttaaattc agaaaacagg tcttgccctt 720
 agcagacaaag aaccacacca gttttcttgc aaggttaacgg atacattggg attcaggagg 780
 gacacagagg tccagccca gaaacttggta ggatttttgtt tgaacactgta gcagatgct 840
 cctccctgccc accccatcaca stagttaggg ctggccatgaa atttotatggc agagtcaatc 900
 ctgcagtcg cttagggatgg gctttttatcccactctcg cacacatcccc agtctatgtt 960
 ttgccttcac agatgtctcc ttgacacccc tgacttaatgg atagttgttgg tttttggatgtt 1020
 qaatttgatca ggtttaatgg atccctgtca ggttggccat agtgggtcat gctgtatc 1080
 tcagcaattt gggaaaggccaa agtggggagga ttgtttggacc ccaggagtcc caaaccatcc 1140
 tggccaaacag agggagaccc ttgtttctacc aaaaaaaaaaaaaaaa aaaaaaaaaaaa 1200
 aaacaatattt ctggacatgg ttgtgcacac tcagtaggtt gagggtggaaag gttccctt 1260
 acatgggaga ctgaagatgc agtgagccat gaatcagccaa ctgcacacca gtagtgagaa 1320
 aaaagtggaa ccctatcaca 1340

(2) INFORMATION ON SEQ ID NO. 52:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 226 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

gcccagatttc cggggtttttgc cggggcccgcc gatgtttcc agagggttttc aagtggaaag 60
 aggagagcga caaagtgaaa atgccccgtg cccggggcgctc cagcggagtc ctgcacactg120
 tcccgccgtg ggttgacgt ctgttattat aagggtgccca tccacctata tgagtacactg180
 acttgtgagg actgacaaact acagcatcag gtacaaaagg tt 226

(2) INFORMATION ON SEQ ID NO. 53:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 611 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

100-010074500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

gcagctgcag cggcagcagc ggcagcagag gcagcagcag tagccaccac tccgcccagg 60
 ccgaaccccc ggctcgccgt cccaggccc cgccgcgtcc gacgtatgg ctgtatgg120
 ggtggacgaa cgctcgcctc tgctgtcage atccactcc gaaatgtca ctccaccgc180
 cccacccgtac ttgcagaaaa gcaagccagg agcggatgg caccctccata tacagccatt240
 gccagtcag acgcgttgg tattccatgtg ataaatcgcc gtgtgtgcac atcaatac300
 aattttgatg gcaagcttca ccagcatgtg gtaaagtgcg cagtgtgaa tgaagctacg360
 ccaatccaaa acccccccaac aggcaaaaa tatgttagat gcccgttgcattttctc420
 attttgttaagg acacatctcg gcaataggc tgcccaagac ccaactgtac acgataatc480
 aacatggcc cagaatgtt tattttgtaa ggaacaaacca gtcagccgt cattgccca540
 tcccaaccag aagggtacaa gggctgtgtg ttggggcacg gttggggaaac acatccctt600
 tggatggga c 611

(2) INFORMATION ON SEQ ID NO. 54:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 689 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vi) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

gccgaccgga cgcagggggc tggcgggAAC gtgaagctcc ggggtgcctg atggggccgt 60
 tggggcccg gtatgttgc ctgttgggg accccctcat tcctgcgtt gccgtccctg120
 ctgcctcatg gggccatcg gagttcaccc gggctgcacc tcagccgtgt tgccgtctat180
 taaggatggc cggggctgtg tggttgcggaa tgatggccgt gaccgatgtt cctcagatgt240
 tggtgttac tcagaaaaatg aagagatgtt tggttgtgcg gaaaaacaaa gtagataag300
 aaatatttca aatacgtaa tgaaagtaaa gcaatccctg ggcagaagct ccagtgtatcc360
 acaagctcg aataatcatcg cggaaatgtt atgttttgcg attggaaaaaa atggaaatt420
 acgatatgaa atagatgtcg gagaagaaac aaaatgtt aacccagaag atgttgcag480
 actgatattt agtaaatgtg aagaacggc acatttgcg ttgggtcg atgcaaatga540
 tgtagtttactgtccgt ttgatgtttgg agaaaagcaa aaaaatgtc ttggagaagc600
 agcttagatgtt gctggattta atgttttgcg attaatttcac gaacctctg cagctcttc660
 tgcttatgg gttggacaag actccctca 689

(2) INFORMATION ON SEQ ID NO. 55:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 560 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

agaaaatgga cgctgacato aatgtcacaa aagcggatgt tgaaaaggcc cgacacaaga 60
 ctcääatacg tcaccaaattgc gcagaggaca gcaaaaggaga ttacttcatcc attctccagaa120
 aattcaaccca tgagcagcat gaatattacc atactccat ccccaacatc ttccagaaaaa180
 tacaagagag cggaggaaaag gaggattgtg agaatgggag agtccatgaa gacatatgca240
 gaggttgcgc ggcaggatcatc cccaaatcattt gggaaatgtcc tggatggat agtaaaaagca300
 gcccgttttttttgcgttgcggaa aaatgttca cagctggtaa tagaaatgttta taatctaggg360
 ttttagccctc ctggagacat tgaatttgag gattacactc agccaatgaa ggcgcactgtg420
 tcagataaca gcctttcaaa ttcccgagga gaaggcaac cagacactcaa atttggggc480
 aaatccaaag gaaagtatgc ggcgttcatc aaaaaaaaaata agctttagtc ccttttacg540
 gggggccat tcagtttcg 560

(2) INFORMATION ON SEQ ID NO. 56:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 851 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

gaagaaggagt aagaaggaca agaaggccaa agctggctcg gagagcgggg ccgagccctgg 60
 agatggggac agtgatacca ccagcaaaag aggtqaatt gtttcttag tagtgaaggc120
 cacttgaagc tggaggagaa actaaagct tattgaaaa acatgttata gatccttttg180
 ttgtctggag agtggaaacat aggttcctaga cagggtggaa agttctggca cattttagct240
 gctactttga gacctcggtc atgttacccgt gtgttgtcat cccatcttg cctgttttaa300
 ggatatgggt ggtgaaagat gaaagaggca gagtttatacc caatgactt tctgttttgq360
 ttggaaaggcc tcacccctaa acccgttaac tgccgcage tgcgtctgt tag tggttgtctt420
 aacatcgtag tccatgttg cattttttaa atcccccttc tttaaaaagggt ttgtaaaaaca480
 aaaaaaaaaa actaaatgtc ctcaagtggaa tgcgttggaa cccataataa gtggtagaaq540
 agtgtcaactg aattttgtct ctgaatccat tataactgg ttttgtccat gctgggtgtct600
 gggttatagg cctgatggc ctggtagtt tccatcttg tctggcttag aggtcagttcc660
 ttgcacttc ctcaaaagtt gtgtacatgt ctccacccat tccatctgtgactttgttcc720
 tggccctct tgggttttaggc ctccgtttact tttaaaaaat gaaattgttc attgtggaa780
 gaagaatgtt gtaattttaa ctttattaaag tcaacttgtt aagttttaa aaaaaaaaaa840
 aaaaaaaaaaa a 851

(2) INFORMATION ON SEQ ID NO. 57:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1354 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

(2) INFORMATION ON SEQ ID NO. 58:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 268 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

cgtgatctt cctcaagtaaa accaagggtgc atttttttgg acccacctat cttgggggtg 60
atttaggagta gaggggttgta aataacttaaa atttttttcc tttctgatata aatttattgtat120
ctcccttc tag aagtccctgtc gtcttttgtc gagaatttt atttaagcat cctttttgtat180
aagaatctt aatgttcctt tttcatccag atctacactt gatgaatccct aaagcttattt240
ctacacagtt cctttatcca gttttccc

```

268

(2) INFORMATION ON SEQ ID NO. 59:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 752 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

TRANSCRIPT IDENTIFIED

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

tgacaaaaga aatggaaataa ttccaaaaaa gttaatgtctt gagaagacaa ccctgaaatc 60
 tattttgaaa agaaaaggca ccagtatatc cagtgtatc ttcatttgcata ttgaatttc120
 ttccaaagtca agatgtaaagaa agagagctatc ttcatgggg ttttaagagaa taaaagaaac180
 caaaaaaagaa cttcacaaattt ctccccaaacaa aatgaaacaa acaaacccaa tgatgtcagc240
 aatgtggatc cataactctc agttttatgtc tgattttca tcctcagatc agatgttac300
 cgtcagccac ttccatgttctt cttaaacacagag ccacagacca agaactataa gagacagaaac360
 tagttttctt tcaaaatgtc ctggccataa taagaaaaat agcacttta ttccaaagaaa420
 accaaatgtttt tggtaatggatc agggaaatgtt ttaatcaaga gcaatgttatc480
 ataaatttttt agatggcggtt cgggaatgtt ccattatccatc tc当地accatc aatgtatgg440
 gatcgacaa agtgcggaaatc cacatgaccc gatggggcgc acatgcgttca tttqatgttga600
 agcagggttccatc acatgcacca gctaatacatc ctgttttgcatc ttctaaagaca tataaagaaa660
 aagtggatgc agatatacattt ccacacacaa agaaaggcca gcaaccggatc gaaggcagca720
 ttccatcttc tttttatccatc tcaaatcttc ta 752

(2) INFORMATION ON SEQ ID NO. 60:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1389 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

1389

(2) INFORMATION ON SEQ ID NO. 61:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 726 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

(2) INFORMATION ON SEQ ID NO. 62:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

ggctggaaaa aatggggggg gacataaac acocacatga aaatacagat tbaaggaaag 60
gaaccaggta agttaggagac agatgttgaag gaaatggaaa ggacatggal20
ayajajaaat jtgctttttt jyaggccatgt ctggaggatc agtgyttagggg agttsaggaa190
ggctgggcct gtgtcccttgc tgtagggacaa gggaggcttgg gtacccgggg ctgtgtgtta240
aaaccctgtg ggcattggc tcatgggtc ctttttgtac atctgttctt ctgtgtgtgtt300
gcctggtttgc atctcatctc acctggattc aaagggttgc atggggatc gtggccatgg gtcctggggcc360
tgaccccccac caaggatgtc ctgtggactg ccatccgttg ctgaacaggg agtataaggaa420
aggcttctt accatataccc tlgctcccaacc ccccaatgg taggcactgttctt gactttttgtt480
ccagaatatac cagaatatcca aaggggctgt tgctgaacag tctggcaggac cagtgcacgc540
acccatctgtt gatgtccaaagg catacaaagg aggcttcaac gctcatgttt ctcttaatcaa600
ggccatgttca gatgtccaaagg aagggaagggtt gtagaggaga aggttgaagc tgtaggttgaaggta660
qactctgtttt cattttttttt q 661

```

(2) INFORMATION ON SEQ ID NO. 63:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1116 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

gggccacact gaggcattc tttggtagaa ttttcaactt gagactaaca caagtatttc 60
cttttctgtt cagttctcca aatgacaaga agtcttttg ctcaattgaa gggaaatgga 120
atggtgttat gtatgcaaaa tatgcaacag gggaaaatac agtcttttg gataccaaga 180
agtgttgtat aatcgaaag aatgtggaga agtttggaga tcagaaacgag tatgaatccc 240
gcagccttgc gaaggatgtc actttcaatc taaaatacag agacattgt gcagcaactg 300
aagcaaaagca caggcttggaa gaaagacaaa gagcagaagc ccgagaaagg aaggagaagg 360
aaattccgtg ggagacaaagg ttatttcatg aagatggaga atgtctgggt tatgtatgaa 420
cattactgaa acgtctttgtgt gtcgccaacgc attagtttg aagatgcaaaa gtttataact 480
gatgatcagg gcagtaggca taattcagca acaaacaatc ttccctttggg agaaaacctgt 540
tcattccatat ctttcaattt cagttgttcc tatctcaggg atactggact ttctgacgca 600
gatgacaaatc taaggggaaa agtttccctt ttccctctgt ggcaagtacg attttgactt 660
cagttcgttgg aaaaacttca gttttttggaaa atcagatgt gtctttctctt ttccaaaca 720
ccacacgttgg aaagcatttta taatccaaatc tctgaaaactc tgccgtctatg tactgtcttt 780
aaagatcacatc aacttgcattt tagttccatc aatctcgcccc acacacatc gtatcacacac 840
acatatacatc atataaaatattt acctgtatgcc agatgtttttt cataaaatattt ctgcctactgt 900
taaatatgttgg ttccctctgttgg ttgtttttaga aaatttagcgc aatgttattaa aatcaagtgt 960
taggaaatgggg catggtttta ctttacataataa cttttatattt ggaattgaac tattattttaaa 1020
ttgtatcttaa ttccctgttgg aatgttttattt aatattttttt agtgcattaaag gtttcataaa 1080
gtatatttttc caaccctttt tttaaaaaaaa aaaaaaa 1116

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(2) INFORMATION ON SEQ ID NO. 65:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 806 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```
tccaaaggct ctttagtctt tcctaagccc cacagtactt tcccgtagtc ctgaggcgttq 60
ggactctctg gggttcttaa cttccctccc cattgtctgag acagtctgag aagaggctta120
ggattttgtc tgtggagat tattcatctg ttctcttat ttaccttccc caaacccaggaa180
tttcaacttc tcaaaacctgc tttgtatctca caacttggagg gaggaaatgtga gctggggggc240
tcatctccac tggctgcagg aacaggccctc cagggtctcc agactgttat tcagacttgac300
aatgatttga caaaaggaaat gtatgagga aaagagaatg tatcattttga acttcaaaga360
gactttcccc aggaaacaga cttttcaaaa gcctcttcc tagagaaaaca acaggaaatgc420
cactcagcag gaataataaa gaaggagaag agcaacacca ttgtatggaaac agtgaagat480
gagacaaagcc ccgtggagga gtgtttttt agtcaaaatgtt caaactcata tcagtgtcat540
accatcaactg gagagcagcc ctctgggtgtt acaggatgg ggaatccat cagctttgtat600
acaaaaactcg tgaatcgatca aataataat tcttgaggaaa gacccttcaa atgtgaagaa660
tttagatggc cctttagtgt tgacttcaaa cttatcaac catcaagaga acaaactgtg720
ggaaaaggct tatcatgtttt cggagttgtgg caaagcttcc agcatataatg agaaaattat780
ttggcatcg agacttcaca gtggggg 8061
```

(2) INFORMATION ON SEQ ID NO. 67:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 226 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

gcggatccgg ctttctgac tgatctttc caagggtgt aagagatggc ggcgggtttt 60
 cggaaaggcg gtaagtcccg qcaqcgggaa cacagagacg gaagccagtg actaccgtaa120
 aaacaacgtt acctaagg tttccggaa aagggtgttg aaaaaaatcc agtgagttct180
 actacaaaat gactcggtt aaactccagg gtgggttaca aattat 226

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2042 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

(2) INFORMATION ON SEQ ID NO. 72:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2980 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

2025 RELEASE UNDER E.O. 14176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

(2) INFORMATION ON SEQ ID NO. 73:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 227 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```
cagcatgtgc ccacggcaca gcataaggat agatccaaag tccacagggt ccattttgca 60
ggtcatattc tgatccttagg aaatgtcctt ttcccatagt tgtcctatgc ctttgggtt120
tagtctatcc cagggtaac tggagaaa tcattggtt qagagtcaga agagcattgg180
ttttggagct ttaatccctt tctggtgtaa ataagggtgt caacttg 227
```

(2) INFORMATION ON SEQ ID NO. 75:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 773 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```

cggaaatgtt aaggttccctg ccttcctcg gccaaggccga acctcttcgc tggcccccgt 60
ggccggaaaaaa gaactttttt ttccggccccc gaaacgttgcg ccggcccaac tcctccggcc 120
ggcttgcggcgc ttaacccttcc ttctttttt ctcttcctcg gtggccggcgat 60
ccttcgtcccc ggccggatcc gttgtgtct gcaaccggctt ctcatacttc tgccggccca 240
acggccgttc cccgttgcg tgatgtgcga caaggatgtc atgtggggcc 60
agacttgat gagggttggaaat actatgttgc caaggggaaa gatgttcaacc tgaaaaggc 300
agatgttggaaagg aaaccttttcc attatgcgcg agatgttggg cagcttggaaa 420
tctgttgcgtt aaaggaggcag attataatgc tccagataaa catccattata 480
gtctgttgcgtt tatggggctc atgtttccgt tgtatggaaaatg cttttgttcaa 540
taaactgttga aaggcccccgg atggacttgc ccgttttggaa gcaacttgaca accagggttcaat 600
caaaggctttt ctccggatgtt ggtatgtatgg actgtataactt ccggaaatgtt gacttcttcgtt 660
tggcccttccat ctgttgttgc ttgttgttgc actttttttttc tggccatgtt ttcaatgtt 720
tacttttaaqa ggggttggggg gagagaaaaat ttccataacaa atccgactac cag 780

```

(2) INFORMATION ON SEQ ID NO. 77:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 870 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

(2) INFORMATION ON SEQ ID NO. 78:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

ttgtgatcg ctatcccttcc cggatcaaca gcgagccccag cccgggtcata tacaaccggc 60
 ccgggaacaa cgtgaaactg aactgcatgg ctatggggat ttccaaagct gacatcacgt120

gggagttAAC ggataaggTCG catctgaagg caggggttca ggctcgctg tatggaaaca180
 gatttttca acccagggA tcaartgaccc attcagcatg ccacaaagag gggtggc 237

(2) INFORMATION ON SEQ ID NO. 79:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 439 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

gtttgggaag tttagatgg gagcataaa ttagggatct ggcaggagga tcatctacct 60
cagtccattag gatttcttaa taaaaaagag attgtatccc tgagttggtt attaaagattaa120
ttaaaattag cccttccttt gaataatgac atcagtttt ctgttctaaa tttaaaattaa180
gtgtttcat cagtagcaca cttccagttt ctataccaa cgactttct cagttttccc240
cttagatgg gacaagtctg ttcaaggggtt catctgttaa gggtcagcag ggggtttggg300
agaggattta agggaaataa cagtgggggc agaatgggtt cgggggttaaa ggttagggac360
aaggggggga ggccgaaagg agggttgaa ggatgggggc ttacactaga tcgggggatg420
ccgggggggc aaggcaagg 439

(2) INFORMATION ON SEQ ID NO. 80:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 2483 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:
- (vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

gaaaaagtct tcaactattt gaaaaagago catagactga gtgcaggcac cagtcgcgtc 60
 ttattactgt gtcaattaaat tggatgttt tgatgtttt gataacttacc ttgtaatgtta 120
 ttttgatgtaa taacttcaag tccaaattat gcccattca atttttttttt ttctatgttt 180
 ttccccccct ttctttagg ctttgttcc tgatgttata gaaaacttc cagtttttaa 240
 caagtccggc tttttttttt atcagatggg ctctgggtt gatctgggtt gtatcccaag 300
 caggggacca aagaacctgg cccaaagaaat gggcatgttga agaggacacat tcgacact 360
 ttacgggatc aaagtgggtc tacaccagt ctgtttttt aatgtttttt tgtaacccct 420
 tggtttccctt aaaaaaaacccg acacggacaa aaaaacttccat atcagaacacat tgatccaaatg 480
 aggaatggag ctgtttttt tgccggaggaa gaaacttggg cttttttttt tgatccaaatg 540
 gatggccagc tccatTTTT ttaatgttga ataaacttccat agttttttt aaatccggaa 600
 gaaaataaaggc tcagggttcc tttttttttt gataagaatggg agaaaggatggc tgatgttgg 660
 gatgtgtgtt agacgtttca cttttttttt tttttttttt ttcttttttca catccaaaga 720
 tattttgttc agaaataccag cttttttttt ccatggaaat gatttttttt tttttttttt 780
 tatgtgttta caaatatatg tcaatgttaca tttttttttt tttttttttt tttttttttt 840
 aatgtgtgtt actaaaaataa gttttttttt gaaagaggaggat gatttttttt tttttttttt 900
 aaacattttta ttcaatgttt tccaaatccat aacgtttttt ttcaaaatggg cttttttttt 960
 atcaatattt gttaaaaactc agaaaggaaatg ctcttttttca tttttttttt tttttttttt 1020
 atgtgtgttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1080
 ttgtgttaat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1140
 gccaatggaa tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1200
 gaaaaacta tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1260
 ttttttttttc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1320
 tattttttgt atttttttat tttttttttt tttttttttt tttttttttt tttttttttt 1380
 ttactaaatcc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1440
 ttaaagttttt agccgttggac tttttttttt tttttttttt tttttttttt tttttttttt 1500
 ttgttgactgtt gggatataat tttttttttt tttttttttt tttttttttt tttttttttt 1560
 ggatataatgg tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1620
 aaaaatggaaa tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1680
 ggacgtttttc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1740
 tcattttggca gggaggaaatc tttttttttt tttttttttt tttttttttt tttttttttt 1800
 actttttttttc gatagatggc tttttttttt tttttttttt tttttttttt tttttttttt 1860
 ctggcatata gaaaaaaaagg aggatttttt tttttttttt tttttttttt tttttttttt 1920
 ttgttgatgtt gacatgtttgt tttttttttt tttttttttt tttttttttt tttttttttt 1980
 atggatataatg agacgttcaat tttttttttt tttttttttt tttttttttt tttttttttt 2040
 gacagtgtaca ttttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2100
 ttttttttgtt gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2160
 atgttaatatac ttgttatttttcaaaatgttca tttttttttt tttttttttt tttttttttt 2220
 ttgttgactta tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2280
 gtggcaatgtt atttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2340
 agagctttttt gattttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2400
 tttttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2460
 aatattttttt atgtatgtttttt aag tttttttttt tttttttttt tttttttttt tttttttttt 2483

(2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vi) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

gggtgggtgggg ggggggggtgt tggggccaaaa gacttcggta tctgacaaca gcatcatcta 60
 cctcagtcat tagggtttct taataaaaaaa gaggttgat ttttgcattt gtatttaagg120
 ttataaaat tagcccttcc ttggaaaat gacatcgat ttgcgtgtct aaatttaaaa180
 ttatgttgtt catcgatccc acacttcccg tttctatacc aagccagatct cttcagttt240
 cccatttagaa tggacatgtcg ctgttcacgc tgcatgtct gtaatgttcc atgcagagag300
 tttggtcata gtattaaaga gaaaatacag tgaggtcaca atgtctccag agc 353

(2) INFORMATION ON SEQ ID NO. 83:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1039 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

cggggataac caaacacagc tgtttacggt ttctccctta acccatgctt tcataaaaccc 60
 ctcggacag ctcccccgtc caggctttct aaccacaccc acccccaggg tgccgcattc 120
 ctgcactca gagtctcgac cggtcctca aaaaacttga ttgtgcata aaaaactctg 180
 gggatcttgt taatcacagc tctaactcaa tagatctggg agatctgcata ttcttaacaa 240
 gtcctccagg aaggcgagg ctgtctggtgt gaggaccatg ctgtgagcag cagggcgaga 300

gtgcggccagg ctgtatataat ttggaaatat caccctgtaa gccatcgctg gccccccacct 360
 ctgtgtgact gatccccca ggttcccccc cccacttctg caaaccggg tattttttcat 420
 tatccacccc atccccagact cccacccca ggttgcctgg tgaagacttt ggccctagca 480
 atttgttgtt ttatgtgact gtgttttaa tcaagatgt acatgtatgc caatctgcata 540
 ttcttacccg tggcaccaca ctgttacatg ccaattttca aaaaaaaaaa actttttctt 600
 agtcttattgg aaagcaaaaata tacaatgtt ttcaatgtt ccgttggata gaaacagtgg 660
 tttaaaggact ccactggccac ctttatggat tggcccccattt gaggctgtgaaat cccggccctc 720
 tgcacccgtg gacccaaccc ctatgtggc caactccaggaa gattttccatc attttttttc 780
 ttcaagaaggc ctttctgtg tgagacccaaat atatttttcaat ctttttgtcc tatccccattt 840
 ttaaaagaaatt agaaaaataaa ccaggccctgt ttctttttccctt ctgaaatccc tgcctctggc 900
 ttcttaaacc catcatctaa ggtgacagag cagtgctggg aataggcatc ttcttttcaaa 960
 ctttcccaaa actggccaca gataggctgg ccatggggaaat ggttctttggaa ttccggggggaa 1020
 ggccaaacgtg ggggatttgt 1039

(2) INFORMATION ON SEQ ID NO. 85:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 330 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

agtgtattca gcaaatgagg gtcagaacctt tcagtttatt gatggttatt cagccgcaga 60
 tgagagttta tgcgtcagcc acttcaattt ctgtaaacag aggcacaggc caaggactgtl120
 aaggggcaga actatgtttt cttaaaaaat gccttaggcat aataaggaaa atagcattt180
 tatttcaagg aaaccatgg aatgtcaaa tgaggaagtt gtaatcaag ggcagtccgga240
 tggatcaatg ggttaattttt aggtgcgtc aaggaggggc ttatattcac tcaaaccgg300
 atgttatttg gtcggccaa ggttggaaagg 330

(2) INFORMATION ON SEQ ID NO. 86:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 235 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

atttaaatgtat ttttttagttt ttaaaatgtc tttccgggtga gggaaaggagc cccaggccaga 60
 aagcaattca atcatggtca agtttcaac tgatgtatct tggatgtggg taatcggaa120
 aaatgaggat ccaaaagaca aaaatcaag acatgtggg tctgtgactg gatctttatc180
 atccatttcta aatccgattt aatattgcgg gtttacaaaa tgccaaagggg gtgac 235

(2) INFORMATION ON SEQ ID NO. 88:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 866 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```
caggaccacgc ctggccaaaca tggcaaaacc ctgtctctac taaaaagtaa aaaaaattag 60
ccgggcatgg tggcttgc ttgtatccc acttcagtct aagttagctgg gactacaggc120
acgtgcacaa agccccagta atgtgggtt ttttgtttag agtgggttgg gccatattgc180
ccaggctgtt cttaaacacc gggggtaaagaa gaattcgcc atcttcgcct cccaaatgttc240
ttagataga ggttggtggc atcgtggccca gctcttgg agtttactaa caattggat300
aacttggggaa agagaatgtt caattccact cagtcttata gaggctctgg tataaggtag360
ccacacatac acttcactt gactttcaac catttatctt tattgtatttgg gaggctgtct420
tctgcgat tttttgtggc tttagatgtt attttgcacac ccttcttcca ctaccccttct480
tacccttaat gtgccaatgtt tgaaacaggtt ttgattttc tgagctactt gttcgcccttc540
tgtgcgttcac caagtaatctt ggttccatctt tctgttccattt catgttattt tcaagtgaaa600
caagacattt tgggggtcaa gtcttcttgg gtgtttgtt tttatgtata taaaaatggaa660
tttttgttcc cctttccatg taatgtccaa ctttatatgg aacttcacat cataatgtaa720
agaagaatgtt aaagccctgtt gtattgtact tcaagatggc tccctgtatgtt atagaatctc780
cttgcataat aaataatgttcc attgtatgtt aacttccca tcaatattaa ttatataata840
ttttagatattt tttaaatacc aacttat 866
```

(2) INFORMATION ON SEQ ID NO. 90:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 846 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

ctccattgtcc aacggaaaaa acatggaagg gtttaagccta aacaaccctc aaacggaact 60
 ttatgcaga aaacaactac ggaataaaaa cccacaaaaa tacagagagg aacgtttta120
 accttttaggg ctcgcgttct ctgccttgg cccatcaggg tcaaagatg ggagtgagga180
 aggaaggat gggacagcat cccctggac gtcaagtgac catcccttgtt ctccacttc240
 cagcctttaga gatgtggacca gccaagacac ctgcgtctggaa ctctcgacc tgctgtttt300
 tctctaccaa ctttggcagg gatcttagat ccatttaatg ggatcgatc ccagtcaata360
 ccattggggc tcaaataatg ttctttagaacc acagatcta gggccagggt cccaaactat420
 aggtgacggg gttcccttc aagctcgac cgaattcggc acgagcgggc acgagcttga480
 agggaaacctc gtcaagatcg atgtgggacc ctggcccttag actcttgtt tctaagaact540
 tattttgagcc ccaatgttat tgactgggac ctgatccac taaatggatc ctatgtccct600
 gccaagggtt gttagagacaa agcagcagggt ctgagatcc agacgagggt ctctggctgg660
 tccactcttc aaggctggag aaggagatccc aaggatgttcc ttgaacctcc cagggatgtt720
 gtcccatccc ttcccttc actccatctc tttgaccctgg atggccaaag ccagagacgc780
 agggccataaa gttaaaaaacg tcctcttgtt attctctggc ttttactcccc tagtgtctct840
 gcataa 846

(2) INFORMATION ON SEQ ID NO. 92:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1374 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

cggaaagcgctc ggactaccgt tggtttccgc aaccttctgg attatcctcg ccaaggactt 60
 tgcaatatat ttttccgccc tttctggaaag gatttcgtcg ctccccgaag gtcttgacg 120
 agcgctctag ctctgtggga aggttttggg ctctctggct cggttttcgc aatttctccc 180
 tggggactgc cgtggagccg catccactgt ggatttaat tgcaacatgaa cggtggaaaga 240
 gctcgtggcg tgcgacaacg cggccgaaag gatgcacaaacg gtgaccgcg cgggtggaga 300
 gcttttggcg gccgcctcagc gcggatcg cctcacagtg ggggtgtacg agtggccaa 360
 gttatgtat gtggaccacg acagcgttgtt cctctggctt ttggccatgt acggaggaga 420
 ggaggatgac atcgccccgtc aaatccactt cagcgtcatac cagtccttcgt gctgtgacaa 480
 cgacatcaac atcgtgggg tgcggcat gcacggctcg ggcacgttcc tggggagggc 540
 ggcccgagacc caggccacca ccggggcccg agacactgat tgatctctgg tcacgaaccc 600
 tcacacggc gcctggaaaga gccacgggtt ggtgggggtt gccagactact gcaagaaaag 660
 cggggcaac aaccagtggg tcccttacat ctcttccatcg gaacgtcgag gcccttcca 720
 gcacgcgaaat gtgttgcgtt gtcggccacaa aaaaaaaaata caataaatat ttgaaccccc 780
 tccccccccc cacaaccccc ccaaaacaaac ccaacccacg aggaccatcg ggggcagagt 840
 ctttggagac tgaagggaa gaggggggg agaagggggg tgacggcccg caccggggc 900
 agagatcag gagctgggg cggccgatca gatggggaaag gggggaccca ggccacgagg 960
 agacaggacc cccgaatcg aggccctggg atggggcaga agccggagtg gggggggacq1020
 ctggccgcctt ccccatcagc gaggttccagc actgtccatc cgggggtggaa gttagactg1080
 ctgcacggccc cacccttcgtt gagactgtgg ctggcgctcg catacgagat acttgggtgtai140
 acttgggtgg tcccttgcgtt caccctcgac aagaccacac ttggggactt gggagctggg1200
 gtcgttgggg tctgttaccc atgtacccca agtttgcgtt ttatagagac aatcttat1260
 gttacttgcgatc cttgttatttca gaccactgtc gagccgatgtt ggaacatcatg atatcttat1320
 ttttatttctt actatgggg cttgttaata aatttctaaa gcctctgaaaa aaaa 1374

(2) INFORMATION ON SEQ ID NO. 93:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 761 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

gcctgatggg ctggagccag actgtggctc gaggaggaga cacagcctta taagctgagg 60
 gagttggagag gccccggccc agaaacgcg agacagacaa aagcgtagga gaagaagaga120
 ggcaggaaag acaagccagg cacatggcc accttcccac cagcaaccag cgccccccag180
 cagccccccag gccccggaga cggggactcc agetctgatg aatctgacct ctatagctg240
 gccccatctt acctcgagg tggaggccgg aaaggtcgca ccaagagaga agctgtgcc300
 aacaccaacc gccccagccc tggcgggcac gagaggaaac tggtagccaa gctgcagaat360
 tcagagagga agaagcgagg ggcacgcgc tgagacagag ctggagatga ggccagacca420
 ttggacactac acccagcaat agagacggga ctggggagga aggaggaccc aggacaggat480
 ccaggccgcg tggccacacs ccccacccctt aggacttatt cccgctgact gagttctctga540
 ggggcttacca ggaaaagcgcc tccaaaccta gcaaaagtgc aagatggga gtggagqgt600
 gggaaatggag ggcaagccca ggaagatccc ccagaaaaga aagctacaga agaaaactggg660
 gctcttccttccat ggtggccacca acaataataa gacacgcacg gcagcacaaa aaaaaaaaaa720
 aaaaaaaaaatcc ttgtttaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa761

(2) INFORMATION ON SEQ ID NO. 94:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1825 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

agggaaagcta gtagcgacc ggaagtgagg caccctcggg ctcgagacag cgccgcacgtt 60
 taagactgag cgacccatgt ccactggaga cggtcagtt ctccactca gctcccccag 120
 cccgagcccg aagacccccc ccccaagaata tctggggggc gatggaaagg agccgagta 180
 gatccgcagg taccagacg cgcacagacg gacgcacagg gagttcccg aagccccgc 240
 ccttaggtgt atcgaaaggc ctcaccatc cgggtggaga accccggagga cccgttccgg 300

 gcggaaaggccc gaccatggct acggccctgg tggcggtcc cgaggtctta cgcgttccgg 360
 ccgcggctag ctggcagggtt gtgcgcggac gtcgcgtgga acattttccg cgagtactgg 420
 agtttctgcg atcttcgtgcg gctgttgcct ctgggttgggt tcgttacccgg caccacgac 480
 gcctttgtat gggcttaaag qccaagggttg tgggtggact gatccctcgac gcccgcgtt 540
 gggcccaagt cctgaaaaggc ctgaatcacc acctttccaga atctggacat atatgtgggg 600
 atccaaaggc tacaaaggcag gatctggaga agattttggg ggccacggaa actttttacc 660
 agcagggtgaa gcacgttca gaggcttgc tggatgttgc ctcgaactcg caggacttgc 720
 aacaaggata tggggaaacctt ttcttgcgtt ccatacgaaa gctgtttttt gagaacttgt 780
 gtcagctgga gaaaggactt cttacaccgc aggacacgaa gtttcaggat gtgtcgatgtt 840
 ggatgcggc tggaggttctt atcacccctt ctcttgcgtt gagacaaat tatgttgac 900
 tgggggtgtt gcttcccgatg tgcttgcgtt ctgactcgtt gaaacctggcgtt gggccatgg 960
 aacagaatcc tcttcaccaa caaaagactt cactccaaat tcccccgtccaa aaaggccaaagc1020
 ctggcacaca tctttcttcgtt ggacccatctt caaggacgc cccagaaacctt ctatgtggcc1080
 gacacccatcc tctggccccc ctaggccgcac gaaaggatcc gtcacaatgg gctccaaatgg 1140
 ggggaggccc taaggagcgc cccacatgtca tgctttttcc ctttagaaat ctccggcac1200
 caacccaggat catatcttaag cttggagacca aggaaagaaca tgcgatataac acagcagacc1260
 tagccatggg cacaaggaga gcttccactg ggaaggttaa gatgtccatgc cagaccctgg1320
 ggggaggccc tcttggaggaa aacccatgtt acttgcgttgc cacagacaa aaggagaaatt1380
 gcttttggatgtt ctacatggac cccctggagac tatcatttattt accttccatgg gccaggaaagc1440
 cagttgttcc tccgttctgt tgcaagcttgc tcatttccatgg gacttgcgtt gtttttagact1500
 ctgtatggaga agaaaatggc caggggggaa gaaaggaaatc tcttggaaaat tatcagaaga1560
 caaatgttgc caccctgtt ccacccatgtt gtgaatctt accccccattt gggccacgggtg1620
 ccataacttgt tcttcctgtt gatctgttgc acatgttgc acctttttgtt gtagactaaal1680
 atgtctctgt tactcttagtc tccgttgc tcaatgttgc aagttagttt gtaggaatgal1740
 agtggaaatgc caggcttggaa ttggcttaactt acatgtctaa aatattttgtt aatccttaat1800
 atttaaacattt tggattttttt aaaaaa 1825

(2) INFORMATION ON SEQ ID NO. 95:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1374 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

ccgggattcc ccctccgggg agcgattgtt cctcgggagg ggccggggagg tggacgcggg 60
 taccggcggt cgtcgggtcg gcagactttg gtcagttggc agcggcaacg gcgcgtcggt 120
 tcggcggtggc ccatgtgtc ctgcaggttc ttccggggccg agggtttcca gaatcaactt 180
 gaacctggcc tttaactgtt tgccaaagtgt ggctatgacg tggctccag ccgcctcgaa 240
 tatgcacact cgtctccatg gccggcggtc accgagacca ttcaegccga cagcqgtggcc 300
 aagcgtccgg agcacaatacg atctgaaggcc ttgaagggtt cctgtggcaa gtgtggcaat 360

 gggttggccg acgagtccct gaacgacggc cccaagccg ggcagttccc attctgtaaa 420
 ttcaacgact cgctgtggat ttgtccctaaa ggcaaaagaaa cttctgcctc ccagggtcac 480
 taggcggggcc gcacccacacc acccccaagacg gcacccacac tgaggccaca cttgtggccat 540
 tccacccctgg agttggaaacc ctggcgctcg agacaggaaag gcaggccgca gtgggtgaaa 600
 catcaggacca ctcccaaggc cccggcttc aacaagacact ttccgttttc tgaaaaaagag 660
 actatgttc tgatgtttca tgcccttttc tgggacaggc ctgggctgtg cagocacact 720
 gteggctgac tttagccccct gtcacttcgat ggtgcctcca ggaaatggcgc 800
 gtcgttccat gaatgtacactt acatccctca ctcttttttc tgccctgttc tctggactct 840
 cccctgtgg qcccaattcc aagacagact ctgcgttcac ccgaatgtta ggcccacatc 900
 tcccaaggctc tttagggagac agaatggaaa cggaggccgc ccctggccagc cgccttgccc 960
 ctggccatctg catatggccgc ttctgtccaa cccttcaggc ccaggccagag tggggatgg 1020
 ctgtgacactt ctggggaggc aggctgtatgg ggcacacccct tggccttcg tccacgagg 1080
 gagaacaccta aaccctgttt cacaatctgtt gggaaatggcactt ctggccctcac ttctgtcttag 1140
 gaaaggccgtt gttgtccat aactcttaacc agcacaggcc tgaggccgtc agtgcacacc 1200
 tgcaggaggc cccttcccaa ggtgtggta ctgtgcctta ctgtacatgc tcggaggccct 1260
 ggccatatacg gagggtgggtt gatgtgtaaa tcaccccccata ctttaatgtaa ttactttctgt 1320
 gagataatcg gtggaaatcc ataqacaaat gaaatccat gatgtaaaaaaa aaaa 1374

(2) INFORMATION ON SEQ ID NO. 96:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2615 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

(2) INFORMATION ON SEQ ID NO. 97:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 508 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

(2) INFORMATION ON SEQ ID NO. 98:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3588 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

tcatgggtgc ggctggcaqt acagtcaaggc tttggaggag ggctgagaag aaaggggcac3180
 tggccaccc ccagggttgc ttggagact gatcacagca gataccatcc caccccttc3240
 tctaaagaac aggccacca cacaataatac ccttcctca cttaactaat gtatcccta3300
 tttggatccca gcaatggagg acaggcagac ttaccccccgt ccatacttagag agaatgttg3360
 tatttttgttgc aaaaacttgc cccccccatc ttccacttgc ttttgtaaad acaaattgtt3420
 aaacctgtga gcttgcgtt cttttctatg ttgttaatcag tttcccttcca ttttgagctgt3480
 gtggggggga agggcattga aattgttagt tgtaatcttgc tgccaaaccaa taaaaaccag3540
 tatttcacac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3588

(2) INFORMATION ON SEQ ID NO. 99:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1218 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vi) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ttgtggcgctt taaaataacaa atctgtctaa gtttaggcaac aggcaugtga cttgattttct 60
 cgaactgtt ttgtcatgaa gacttgtcaaa gagaaaaaat tgatgggact cttgggtgtt 120
 gtatttgtat agtattttgg tgaagagtcc ctctgaagtat tgggcagcat tttggagaca 180
 ctgaaaggccca ttgttaatgt catgtatgt cataagatgtt ctccaccaat taaaagatctg 240
 ctgccttagac tcaccccccattt cttaaaaagaaac agatcatgaaa aagtacaaga gaattgttatt 300
 gatctttgtt gtcgttattgc tgacagggtt gctgttaatgt tatctgtcaag agagtggatg 360
 aggatttgtt tgtagctttt agatgttctt aaaggcccca aaaaggctat tctgttagagcc 420
 acagtcaaca cattttgtta tatttgcattt gccatggcc ctcatgtat attggctaca 480
 ctctgtgaaa accttcaaaatgt tcaaaaaagg cagaacaggag ttgttaccac tgtagcaata 540
 gctatttgtt cagaaaaatgt ttccacccctt acatgttccctt ctgcctttaat gaatgtatc 600
 agatgttctt aactgtatgt tcaaaaatgtt tggtttaatat cggtttccctt cttgtttgaa 660
 tatatttgtt aaatgtggaaa agactatcatc tatgtccgttac caccgttact tgaatgtct 720
 ttaatgttata gagacccctt acacagacac acggctatgtt cagttgttaca gcacatgtca 780
 cttggggttt atggatatttg ttgttgcattt tcgttgcattt acttgttggaa ctatgttatgg 840
 cccaaatgtt ttgagacatc tccttcatgtt attcaggcag ttatgggagc ccttagaggc 900
 ctgagatgtt ctatgttgcattt atgttgcattt ttgttgcattt gtttacaggg tttgtttcac 960
 ccaggccgtt aactgttgcattt tggttgcattt acctccatctt cattgttccctt 1020
 caggacgttcc tcatgttgcattt ttacccatgtt atctacaaatc atgttgcattt ccacccatata 1080
 atccgttgcattt tgaacccatgtt cttatgttgcattt agttaatgtt atgttgcattt tttgttgcattt 1140
 aatgtccatgtt gtttgcattt ttgttgcattt ttgttgcattt tttaaacatgtt 1200
 cayatgttgcattt 1218

(2) INFORMATION ON SEQ ID NO. 100:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1303 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

(2) INFORMATION ON SEQ ID NO. 101:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2333 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

tggaaaatgc	ggacagtata	ttcagaaaagg	ctattccaag	ctaaagatat	ataatttgta	60
actaaaaaat	gttagcagaat	tttggggcgtt	gacagacttc	tcagatacgt	tcgaatgtta	120
ccggggcaag	tcggatggaa	atggaaatccc	ttctgttgtt	ggagatgtta	agggttcgtt	240
tcggatctac	cctctggccgg	atgaccggcc	cgtgcggcc	cctccagac	agtttccgggaa	300
attacatggc	agcgcccccc	aggatgtcgc	gtttaggttt	tatcatgttc	gaggctttaga	360
gtcccgcccc	caggacaaaca	atggccctgt	ttacccctac	aaaaaaataa	catctggggaa	420
aaaagtccat	gaagaccggg	atcaactatc	tcccaacact	ctcaacccag	tcttggccag	480
gtatgtacgg	ctgtcgctgt	acttacatca	aaaaaaagac	ctggaaaattt	ctgtgttttt	540
ttatgacacc	ttttccgggg	atggaaaaat	aggagaacaa	attatgtatc	tgaaaaaccg	600
attcccttcc	cggtttttgg	cccaatgcgg	cataccaggag	gagtactgt	ttttctggagt	660
caataacttg	cgagatcaac	ttagggacac	acagctgttt	caaataatgc	ccagatccgg	720
aggcttccca	caaacccatc	ttttccggaa	ttggggatga	atcatatgt	gaggacggaa	780
ctacagcttg	gatgaatttg	aaggccaaac	aatctctgcac	cagcacccctcg	ggggccccctga	840
agagqggctt	gtcttcacaa	tccttccgggg	tcaggggctt	gtccctggac	acgtggaaac	900
aaaggatttt	cacagccactt	tccggccccc	cattttcccg	ggaaaaactt	atgttggttt	960
ggatgttttc	cccaagggat	ttggggccacc	aggcccttc	ttcaacatca	cacccggaa	1020
agccaaagaaa	tactacttcg	gtgtgtatcat	ctggaaacacc	aaggacgtta	tcttggacgat	1080
gaaaaggatc	acaggaggg	aatgggtga	catcttcgtc	aaagggttgg	tttctggcaal	1140
tggaaaacac	aaacagaaaa	catgttccaa	ttagatattt	ttggatgttg	agggaattt1140	1200
taacttggcg	ttttttttcc	cggtttacta	ccttcaggcc	gaaacaactt	gtatctgttc	1260
gaaaaaaaaa	cattttctgg	gttttgcacca	aaacggattt	cgaaatccac	ccaggctgtat	1320
cattcagata	ttggggcaat	aaacttttcc	ttctgtgtac	atcttttttt	ttcttgcata1320	1380
tgactgtcg	cacacgtata	ttccctgtccaa	atccacaggag	aaatgcgggt	ttggatcat1380	1440
tcggggacct	aaaggccatg	aaaccccttac	ggcccaagaca	gcttccttcc	tttgcacgaa1440	1500
gtccatgaaa	ggatggggc	catgttacgg	agagaaatgt	ggggcccggt	taatgtgtt1500	1560
gaaaatgggg	atgtacatcc	aaatcttcgg	cgagggggaa	ggccacggaga	ggccagccgg1560	1620
gaaggggccg	gacggacccca	atggggccac	aaagctggac	tttaccaatc	gaccggaaac1620	1680
ctcccttcctc	ttttttccca	accctatgcac	gacatggatc	ttcatctgt	ggccggccgtt1680	1740
taatgtggcc	atcatcgctt	ttgtgtttcc	gtttatcttcg	ctgtgtttcc	ttggccgttgc1740	1800
ccttcacttc	tttccggaaat	attttgttcaat	ggatgttttt	aaaggccatc	tttgcacaa1800	1860
gcaaaaggctt	catttcggaa	gttcatccgg	aatggagaaa	ttctgtccct	gttagaccaac1860	1920
atccggatgt	atttttgttc	ttggggatggc	cccccactgg	agttgttgcoc	atgtccacgg1920	1980
ggccccatgg	tttccgggggg	ttttttttttcc	ttttttttttcc	ggcccaaaatc	caatgttttt1980	2040
atcatgttat	cttttttttt	tttttttttttt	tttttttttttt	atgtttatgc	ttttttttatgc	2100
aaatatatttt	tttttttttt	tttttttttttt	tttttttttttt	ttttttttatgc	ttttttttatgc	2160
tcttagacttc	atgggtttgg	aaaaatggtaa	tttttttttttt	ttttttttatgc	ttttttttatgc	2220
gatataacttc	atattttgtta	tttttttttttt	tttttttttttt	ttttttttatgc	ttttttttatgc	2280
gtttagaaacaa	tttttttttt	tttttttttttt	tttttttttttt	ttttttttatgc	ttttttttatgc	2333
agtcttattt	atcccttttt	tttttttttttt	tttttttttttt	ttttttttatgc	ttttttttatgc	

(2) INFORMATION ON SEQ ID NO. 102:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1377 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

cattactgtt atatgaaaaa catttttagt atttaataaa aggataatgt ttatTTaaaa 60
 aacctgactt ttccagaga attttggttt gcacattcat gtttattgaa gtggactaat 120
 ttcatataatg caaatcagag ttaaatatta aaaatttgtt aaatacaatt gacataggaa 180
 ttacataaaat attagggaa gaaacaaggaa caaattttaga ctttgaaatcc gaagagataa 240
 agcttacttg actttcaat ggagatgtq tgaaaaacca ctccattcagt ctttcagaa 300
 aaaaagcacg tcatctgata agagtatgac atggatggaa tgccctacag gggcTTgga 360
 catctttat ttgcgtcat atgtggaaatggatggacttt acagataatg gagcagaago 420
 caacataggtaaaaaggatcc caaactcttcc cccatataatg tagaaacatg tgaaagtaca 480
 ataaactctt tgttcaataccagcatca gagagttcc catttgcata tagaccttga 540
 atttatattt attgatcaag ttctaatttt tatgttatattt ttgtgcataat tcaccaataa 600
 caqttaaaaat taattatgtt ttatgtttaa tatatgcacc taccttttcc cgtttagtgc 660
 tcagtaaaatg tgttatTTT tcatttttcc aaaagagatgt ttgttagttt ccctgttagt 720
 ttctccctta tagctttttct tctgataacc atgactttcag gagctttaaa actatctato 780
 ttgcattttgt gtctggcgga gaactagccca tcaagcttcc gaagcttgcc atcattgtta 840
 attttggggac tgggctgtct tggggctcag aaggtaaaga actattttag cagatgtgt 900
 tgggtggcac tggatccac ccaactgcacca agttatgtt gtttagatgtt tcattttaca 960
 acacaaaat aagctgtgt caaaatgtttaaaaatcatgg aaaaatggaaa tcttagaaagat1020
 ccttagagaa ccagccaaacc aactcttcta ttttaaaagt gaaggattca tagcacaat1080
 tacttgccta agatcatcca ggaacgaga caaagaaatcc aatgtacttgg gggacaaga1140
 tttagccccca aatttcgtt tttttcttagt attaaacattt gccccttccg acaaattttg1200
 gatttcaatc ttgtatattt tctgataaaacc tgctgatattttaa gtttagatgtg1260
 cattagatyt tagatagcgt gcaacgtatgtt agatacttgc ctaagacatgttccctgtt1320
 ccagcagcaa tcttagatgtt gttgcacgtt gtcattgttgc aatgtataaag cagatgtt1377

(2) INFORMATION ON SEQ ID NO. 103:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

ataaggaaatg agaaggaaaagg ctgtgttcta tcaagtaggtg agatggaaact ggtcctggta 60
gtgttgagc aggacagggc ctttagttctg atgctgttgtt cctttgttat agtagagocac120
cggggttaac caccactcct ttaggtactt tgtagtgaca acagaagttaa aatatttcaal80
ttatattaat tagaaatgtta tgttttactg gaacctgcaa tatgcatgtt cagaatattaat240
aatttttactt cttttgttca agttatacta aggcaaaagcc agtggattca aaagttagac300
attgacaggc cattt                                         315

```

(2) INFORMATION ON SEQ ID NO. 104:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2355 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vi) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

(2) INFORMATION ON SEQ ID NO. 105:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1339 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

(2) INFORMATION ON SEQ ID NO. 106:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3751 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

(2) INFORMATION ON SEQ ID NO. 107:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

cgctcgcccc ccgcggagaq atcggagggt acttggccaa gagtctggcg gaaaagctgt 60
 atctatgtca gtacccctgtg cgtccagcct cgtgacacta cgtgacatt ccgcacccct120
 cagccaaagat caagccccaaag cagcagaagg tagagttga gatggccatc gacaccctga180
 accccaaactt ttgcggcagc aaaggggagc agattgcgt gaaacgtggac ggggcctgcg240
 ccgcgcgagac cagcacgtat tcctcgaagc ttagtgacaa gcagaccccttc tgctttccc300

(2) INFORMATION ON SEQ ID NO. 108:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1465 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

ggccaccccttc	cctccccccaa	ccctggggcc	gccccagggt	ttctgcgcac	tgccgttcc	60
tccctgggtgt	cactggcagc	cctgtccctt	ctagggac	tgccaaggac	ttcttcgttag	120
gctggggagg	ggtgagggt	ctcaaggcaa	cgctggccc	accacggagg	ggcaggagca	180
ctaaacatgc	ccttagcttg	cttccctctt	ccctcccttt	tatttcaag	ttctttttta	240
tttcccttctt	cgtaaaaaacc	ttcttccctt	ctgcacaaat	ggccgttacc	ttacccggccc	300
cgccacccctt	ttgtcacccc	actttggaaa	cacacagtgt	tgccagggtt	ccacgcgtat	360
cgccaccccttca	tctcccttct	tgtagccccc	caaaaggccc	ccaggcaaca	ttggggggccc	420
agtccagagag	ccggcactct	cagtgtccct	ctgggttagt	ttggggggcc	ttctggggggc	480
cgtggcttgt	gcatgtggcc	tgctgaccca	aaacacagag	ctggagacgg	tcaggagaga	540
gggtggccgg	ctcgaggggaa	caggaggccc	ctcccccggat	ggggaaagggt	atccctggca	600
gatgttcccg	gaggcaggat	cgcgttccct	qgaaggcttgg	gagagtgggg	agagatcccg	660
gaaaaggaggaa	gcaatgttca	ccccaaaaaa	haaaggaaag	cacttgcgtt	tgccacgtt	720
tccatccataac	ggcaccccttca	aggatgactc	cgtatgtaca	gagggtgtatg	ggcaaccaggc	780
tcttaggcgt	gggagaggcc	tacaggccca	aggatgtatgt	ttccggcaatc	aggatgttgg	840
agtttatcttcg	ctgtatagcc	aggtcctgtt	ttcaagacgtg	atttttccatca	ttgggttggat	900
ggtgttcgtoga	gaaggcccaag	gaaggccgga	gactttatcc	cgatgtataaa	qaatgtatcc	960
ctcccaccccg	gaccggggcc	acaacagotg	ctatagccga	ggtgtttccct	attttacacca	1020
aggggatata	ctgtatgtca	taattttcccg	ggcaaggccg	tttttttttttt	tctttccacca	1080
tgccaccccttc	ctgggggttt	tgaaatctgt	atttgtttat	aaaaaaatggc	tcccaagcttg	1140
gaagaccagg	gtgggttacat	actggagaca	ggcaaaagggt	tgatgtatgg	aggagggggal	1200
atgtgcaggaa	acaggccgtt	tttccctgggt	ttggccctcc	tttcttcact	tttccctttt	1260
cattttccacc	cccttagactt	tgattttacg	gatatcttgc	ttctgttccc	catggagctcl	1320
cgaattttctt	cgtgtgttga	gatggggggc	ggggggacggg	cgccggcgtt	tgccacggac	1380
tgggtggggc	ccactggggaa	cattccagac	agcaccacca	ttaaaggcc	gtccggggaa	1440
aggccacccggc	gggtttggggc	aatgtc				1465

(2) INFORMATION ON SEQ ID NO. 109:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1488 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

cggccggagg	agcaggatgg	agatccctgt	gcctgtgcag	cggctttggc	tgccggcgcc	60
ctggcccccc	ttggccggac	tttcggccgc	cgaggccctc	ttttagccgc	gttccggcga	60
gggggtctgt	gaggccggc	tggctggct	tcgtcccccc	acgtccggcc	ctactaacct	180
gcgcgcaccc	agcgtggcgc	tgccctggc	ccagggtgcgc	acggaccccg	gcacactttc	240
gggtgtctgt	gacgttgaa	acttctggc	ggaggaaatt	gtgttcatagg	tgttgtggcga	300
acacgtggag	tggtcggcgc	ggccaggaga	ggccggcgat	gacggccgt	tgtcgccggc	360
cgaggctccac	cgtgtcgatc	gcgtggccgc	tggctgttat	cggtgtccgc	tgacgttcgc	420
gtctgtcccc	gaggggcggtc	ttgtccatcca	ggccgcacca	ggttgtccgc	aggccccacc	480
ggccggccga	ccggaaatgg	aggggggctgg	ggccggccgc	cacccgggg	gccttcctcg	540
gtccgtttttta	ttaaaacggca	tgtgtactcg	ccaggccgca	tgccggagat	ggcccaaaagg	600
ctgttccttc	accacatct	ggatgttcgc	tcgtacccca	tcgtggacac	tgcttcgttgc	660
acatagaccc	ttccactgtac	aeacctcgctc	tcagagcccc	tcacagtttc	cgaaaaaccaca	720
ccggadaactc	cccccgttcc	agacccatcc	agactacacc	taacccttgc	cgccagatgt	780
cggcccccac	gaccacactt	cttggcatat	agccccca	aaagccccctc	cttctactcc	840
ttctgtgttc	tctacaaaaga	catccgggtt	ctacattttc	atccctttcc	tatttttgaca	900
ccaaattttat	gtgttagacag	ccctggccca	acccaggccc	agtccaggcac	aatccccccca	960
cccccccaac	gtcttgcgtt	gcacagact	ccacttcacg	ccatccagg	ctgtttttcccl020	1020
aagacccgtat	cttttccctgt	caacccggaca	gtcttaacat	gcccccttca	gccccattttc	1080
ttccgtgtaaa	ccccccggat	ccacccagg	cttgggaccc	cttttttgcac	tgcccaact1140	1140
cttggatacc	aggccaaact	gaacacccaa	cacccaaact	tcacagactt	ccccacccaa1200	1200
cctccggccaga	cttcgtccacgg	atgttcctagg	cccccccttca	aacttttaccc	agccccccatc1260	1260
cccttaatgtt	ctttttgttt	gaccccccgg	ttttttttttca	gatatcttcg	gaaacccaccl320	1320
tcctccatctt	cttccttttt	cttcgttgcac	ccacttgac	acccggcttg	atccccccacal380	1380
gcctttttcc	ctggccacac	tcctttttgttc	ttttccaggc	ttacttttcc	ataataatgtgt1440	1440
cttagactttt	ggaaaaaaa	aaaaaaaa	tggtggccgg	ccggatgt		1488

(2) INFORMATION ON SEQ ID NO. 110:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 783 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

aacatattgt taaaaggtaa ttttagagaaa atatgaagaa ctgaggagga aaaaaaaaaa 60
 aaagaaaaa accaaacaacc tcaactgcct actccaaaat gttgtcatt ttatgttaagl20
 ggaagaatc cagggtatgg ccatggagtg tacaagtatg tgggcagatt ttcagcaacl80
 tcttttccca ctgttttaagg agttagtggg ttactgcct tcacttcata atccagtagg240
 atccagtatgat ccttacaaatg tagaaaaacat aatcttctgc ctcttcata tccaactaa300
 gccttactct tcttgaattt ttaacctatg atatttctg tgccctgaata tttgttatgt360
 agataacaag acctcagtgc ctccctgttt ttccacatTTT octtttcaaa tagggcttaa420
 ctcaacactc cggtttagt cagcagcgtc cctcaagacc aaaaatggaa tattccatgac480
 ctaqtttcc atggtgtttt ctgactctga gtcacagatg ctggtaaagc tcacttcgg540
 gcttcatctg gcaacatTTT tatccgtatg gggatgtttt gacactagcc caatgaatg600
 aattaaatgt gaccatagg jctgagctct ctggggctg gcaactgttgg aaggccagctt660
 tccctgcctc tcatcaactg aatgggtca gcatgtctat tcagcttctgt ttattttca720
 agaaataatca cgctttccctg aatcccaact aatccatcac cgggggtggg ttttaagtgg780
 gct 783

(2) INFORMATION ON SEQ ID NO. 111:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1045 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

tctgttctgt ggacaactgt tactgttctt ccgtggccaa ccatggcgcc caccagccct 60
 acccccgcgc cggcactttt ccctggacag tgccctcgca ggagttactca caccggctcc 120
 cggccacacc ctcgggtcccc cagtccttc ccagcttgc ggtcagagac tggcttgacq 180
 cctcccaagca qcccgccac caggatttct acagggtgtt tgggcagccg tccaccaaac 240

(2) INFORMATION ON SEQ ID NO. 112:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1386 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

cacactcact	gccccatgaag	gaagaggggg	caagtgtacc	gaggaagggg	atgcctcaca	60
gcaaggaggc	tgcacccatgg	gttttcgtacc	cattcgctcc	agtggagggc	agggttgcggc	120
ggaaacaaaga	gagatgggg	ggcaaaacgc	cgcggccac	ggcacccgca	gtgttaatgc	180
agaggagatc	aaggtagccc	gtattcatga	gtgtcagtgg	gtgggtgggg	atgcctccaa	240
cccgatgtcc	ctggctgtcac	acaatggatg	cgtggaaagg	ggagaatgg	gtcaaggagag	300
tttccacagag	tcgccttcag	aggagtggaa	gggacaaat	gtgtcaatgc	tttcttcgtaa	360
aaaagccaaa	gggtttatagg	ggtacactta	gggggttgc	gcaagctgtt	acccaaaaat	420
ttttaaatgt	ttttttaatt	tgaataataa	aaccaggaga	aatgcataca	gggcatacg	480
aactggcga	aaacctttgt	gacatgaat	gttccatgt	gaaattttgtc	ttttatgtat	540
taataaagat	tacaaaagaca	atggcatact	tggggtgaga	gggagctgtag	gtatgttgcg	600
gaggaaatag	tattgcaggg	aacatgtaga	aaacatgtgg	atgcacgttt	ttagatatact	660
ctgcactttt	caattgtca	atcttttgt	gcactttta	gtttttata	tttttgttgcg	720
aatggaaatgt	tatactgtaa	gtcttacactt	actatctact	atgcctactt	cacccatcttc	780
taaggactcg	gcattttgtcc	acagtcaac	tccaaagagag	ggtaggtgtat	aaacactgtac	840
ccgtgtctgc	tgtagcccc	acagaggcaa	tcatgcccc	tagattcaag	aaagacttaag	900
cggaaatgg	gggttggaaagg	tgtgtatgtt	ggggatctgt	ggggctttgtt	ttccatcttcgc	960
taataatcc	tttataat	atcttgatga	ttttttat	ttaatcacaat	ttgcaggaaal020	
ttcagatgtag	gcaagaaaaat	tttattggcc	tgggtaaagac	tggaaagcatt	ccaaatttag1080	
cttagactgt	gcaaaagggt	tagctaaat	actcgatgt	aaacccgtca	ataaaaacaa1140	
cattatgtta	acatgttactg	catgcacago	actgtgttgg	gttttagtaat	aaaaaaaagat1200	
aaagataatgt	gtctttgtca	gcataaaat	aaagggtccaa	gggaatattaa	tctggaaaggl60	
aacatatgcc	attttttaaa	ctatgcacgc	tttttttttc	ttttttccat	caataggc1210	
cggggttcaat	ccccagaaagg	cacaaaatga	atgaaataat	aaataaaatga	ataaaagacaal390	
aaaaaa						1386

(2) INFORMATION ON SEQ ID NO. 113:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1747 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

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ccagtctgtg agccctgtc ctgtgggtc ccaccgtctg tcgcataatgc agtggcaact 60
ggagaggac acacatcatga aagtgaatgt aaactcgat gtctggaaagg ttatcatgtat 120
gatacagata cagataattatc caccctgtcga aagaatgtgc gctgtttccc tgagagaatc 180
tccctcgaatc ctaaaaaatc tcccttcggc gaaaacatata cacatataatc tggatcatggg 240
gacgatttca gtgtgaatag gcaagtttct gtgtcatgtc cagaagggtt taccttttag 300
ggagttaaca tatcatgtatc tccatgtatg ggaaccttggg agccaccattt ctccgtatgg 360
tcttcgaatc cttttttttt tggggaaacctt gaaatgtccaa aacatggatt tggatgttgc 420
agtaaaataca cttttttttt gaaatgtccaa aacatggatt tggatgttgc tggatgttgc 480
gggaacacggg aacgtgttgc caggagaaac agacatgttgc gttggggggggg ggcaatatgc 540
aaaagacatca gttgtgaatcc tccactttttt gggaaatgttgc cattttttttt 600
aggacacgtt gacccaaacgtt ggttatattcc tgcacaaacgtt gcttacatgtt tggatgttgc 660
tcttgaggccatc actggacacaaatggaaacc tggggccacc cttttttttt ctggaaaccca 720
aatccatggc ctgtttttttt tggatgttcc gagaatgttc tgctgttgc aaaggaggttt 780
tatgttgttgc aagatgttgc catcaatgtt gggaaatgtt ttctgttgc gggccacggc 840
atccatcaatc gcaacccccc cttttttttt gggccacggc acacatgttgc gggccacggc 900
tcatgtgttc caccatgttgc cttttttttt gggccacggc acacatgttgc gggccacggc 960
ggagacatca atgttgcattttttt gggccacggc gggccacggc tttttttttt cttttttttt 1020
gtttttttttt gggccacggc atgttgcattttttt gggccacggc gggccacggc tttttttttt 1080
ccatgttgcattttttt gggccacggc cttttttttt gggccacggc tttttttttt 1140
atggggccgc tttttttttt gggccacggc atttttttttt gggccacggc tttttttttt 1200
gtggcccccc accatgttgc tttttttttt gggccacggc tttttttttt tttttttttt 1260
gttttgcattt tttttttttt gggccacggc tttttttttt gggccacggc tttttttttt 1320
ctttttttttt gggccacggc tttttttttt gggccacggc tttttttttt tttttttttt 1380
caccatgttgc tttttttttt gggccacggc tttttttttt gggccacggc tttttttttt 1440
tggacttgc tttttttttt gggccacggc tttttttttt gggccacggc tttttttttt 1500
tggacttgc tttttttttt gggccacggc tttttttttt gggccacggc tttttttttt 1560
atgtttttttt gggccacggc tttttttttt gggccacggc tttttttttt gggccacggc tttttttttt 1620
gtcttacatc cttttttttt gggccacggc tttttttttt gggccacggc tttttttttt 1680
ttttttttttt gggccacggc tttttttttt gggccacggc tttttttttt gggccacggc tttttttttt 1740
aaaacccgc

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(2) INFORMATION ON SEQ ID NO. 114:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1526 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vi) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

cgagccccaca ggccccggag tagcagcggg gaggccggg gcccgccggc cggagccgc 60
 cggcgccggc gtggggcgtg cggggccggc ccatctcggtt gggcgaactt agctgttggg 120
 gcgcgcgggg aggccggcca ctccatgttc cggacggcag cggacggcag tcccaacaa 180
 gcacgcacag ctccacggat tacagcggca gcacgtttccg cagcggcaat tgccggcaga 240
 gcaatgttgc acgttgtccca agctgttccca gcacgtttccca ccacaggccc tggtccatgg 300
 tgtcgccggg ggtccccccg agcggccaca gcggccggc ttgttttttttccaaatccccc 360
 ctccatgttc ctccatcaagc gtccatcgcc gcaagagatgtt tggttttttttccaaatccccc 420
 aggactggac cagtgttggaa tgccaccaggc cagcttatgtac actggccgttcc tccatccatgg 480
 cacacacaaa ctgggttaacc tcgggggtca tgccatggca ttcccccggcc tgccggcccc 540
 cagccatcca ccccccacaaac tgccacttcc aaatttttttccaaatccccc 600
 tccggccatcc tccgttgggg ctcccttttttccaaatccccc 660
 cttttttttccaaatccccc 660
 ctccatgttc ctccatcaagc gggaaatccccc aaaaaaaaaaaaaaaacccggccac 720
 aaaggatgtt tccatgttccaaatccccc 720
 tggaaggcc gcaagggccc ggtatggacac accggaaatccccc 780
 agaggacatc gccaaggaaaa aacggccatcc acggatccatcc 840
 cgatgttccaaatccccc 840
 cggatgttccaaatccccc 900
 gcaatgttccaaatccccc 960
 gcaatgttccaaatccccc 1020
 ccacacccatcc 1080
 ctggatgttccaaatccccc 1140
 ctggatgttccaaatccccc 1140
 cggatgttccaaatccccc 1260
 ctggatgttccaaatccccc 1320
 gggatgttccaaatccccc 1380
 ccacacccatcc 1440
 atgttccatcc 1500
 atgttccatcc 1526

(2) INFORMATION ON SEQ ID NO. 115:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1205 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

cccgagaaaa accaatttaa tgcttctgtt cttagcattt cacagcatgc aggactcaaa 60
 tggatacaac agaagaaaac aaccacaaat ttttggaaaa ccctttgtcc aatgatccat 120
 attttgatat ctattgacaa tcccttagaa ctttaaatct caaaaacaaa aaagtactgt 180
 ggatctccct cgaggccaaat tcggctcgag ggccgtcacc tggagatgag aaaggccccg 240
 gggtggggacc atgttgtctgt gtcccaacag cagccgagag gcggggagga cgctgtccg 300
 caggagccca agagccagcc agagccagag ctggggatca aacgagctgt cccggggggc 360
 cagaggcccg acaatgccaa gcccaacccg gaccttaaac tgcaggctgg ctccgactct 420
 cggaggccgac ggcggccacct tggccctcat gcagagggtc agctggccccc gaggatggg 480
 gtcatcatttgc cctttaaccc cctgcctgtt gtccagggtga acgactttcg tggcgccctg 540
 gatgcccaacgc tccggccaggc tgccggggga gctctgcagg tggtcccacag ccggcagctt 600
 agacaggccgc ctggggccccc agaggagttc tagcacccgt tgcccatggag ggccacccca 660
 gccactgccc tcctcggcca gcagccaggc tgctctcagcc gcatcccaacg caaactctgg 720
 aggtcacact cgcctctccc cagggttcca tgctctggc ctcacccaaag tttgtgtggc 780
 agtatadaaaatg attcacatgttgc gcatctttc cagaatgttc ttgtgtgtcgt tctgtgtccg 840
 ctcttagttt gaggctctttt gaccccttgcg ctcgtggcactt actccacccgt tgaggaggaa 900
 acggccctccg ctgcggagatgt gctgggtgcac tcccaagggtc aggctgggggaa gctgtgtgggt 960
 ctgtgggtcag gcttcctgttgc cttgcacaggc agcaccgggtg gttttgggt tgagctccggc 1020
 cttgtgggtggaa ggttgcgttgc gttgtgttgc gttcccaacac aggctactgt gagagccagc 1080
 atccaaacccca acgtttgcag tgacttcgaa tgataattat tatgtactgtt tatcgtatgtt 1140
 tcccacatgttggtagaaatg tcttgcataaa acacttttgc cttcaaaaaaaa aaaaaaaaaaaal200
 aaaaaa 1205

(2) INFORMATION ON SEQ ID NO. 116:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3968 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

(2) INFORMATION ON SEQ ID NO. 117:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 798 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

gtaatggaa atttgggtgt ctgaaatcttc ttccctaggat attgtatata tccacgttc 60
 tagtggtat tctgggatt ttacccctgtc catgtttgc ccttaggtac tagaaaggagg120
 agatgttcca aacttagca tttgtttccat ctcgtttaga agtggaaatg tcatacaggaa180
 tagcaaacac ttctgggtcc tttttggcca ggcttggcca gagccggcaa cagcaacaaa240
 atgtggaggaa tgcaatgaaa gagatgcaaa agcccttgcg ccgttatatt gatgacgaaag300
 atctggatag gatgttaaga gaacaggaaa gagaggggga ccctatggcc aacttcatca360
 agaagataa gccaaggag aacaagaata aaaaagttag acctcgatc agtggtccag420
 cacccctccctt caacagattt aatatctgc ctggatcatc ctggacacgga gtggacagat480

 ccaatggatt tgaacagaa cgctttgcgaa ggcttgcacg caagaaggca gtggaggaaac540
 ttgccttcaaa atggatgtt gaggatatgt aactttccctg aggctgtggg ggtggctggg600
 ctgtggtagt gggcatggc acgcagatcc ccaagtgttgc cagtgtctg tgtaataat660
 tggagccccac acagacccacg aacctttgttgc atgcctgtt tgaccacaga agaatattcg720
 agacctgtat tttggatgtt ggtacctgtt ctctttggg tggacacgc acgcgtgttt780
 ggtgggtttt cagaggaa 798

(2) INFORMATION ON SEQ ID NO. 118:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1068 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

cccctcttcgtc tgacttcgtc tctggacgtt ttaataacgtt ggtgtcccccg cgggatcaaa 60
 ttccagcttc acatgttgggg actggcttcgtc tggccctgtc tggagagacca tgaacagggtt 120
 gtatgtgaag cccttggaga ccaggatcttc caaagtcaaa gccaagacca ttgtgtatgt 180
 ccgttgcacttc cagaatgttgc actttggatgttgc actttggatgttgc ctaaagagcc agttacaggc 240
 ccagaccaaa gcttttcgtgt tcttgcacca ctcaggatcacttggagaa agggagatctg 300
 cttgcaccaaa atcaaggatc acgacgtttgttgc agaggatgttgc agccccacag gcccgcagg 360
 agagaagggg gaggcaaaatg acgacgtttgttgc agaggatgttgc agccccacag gcccgcagg 420
 gacccaaggd cttcaggggc tggagaagac cctgtgtgtc acgttggatgttgc tgcacggcgc 480
 ccgcacccat cgttgcgttc acgttgcgttc ccaggatgttgc cgggacacgca agaaggatctt 540
 gtggggaggat ctggaaatgttgc tggggaggatgttgc ggtgtcccttc atctatcaga agtccaacg 600
 gcaggaggat gagatcttcgtc agaacttggatgttgc gaaatcttcgtc aaaaatgtcaga aaacgcagg 660
 gaaatggcccaaaaatcttcgtc ccaaggatgttgc gcaaggatgttgc catggacacg cccgcctgtcc 720
 ggaggacttgcgaa gagatcttcgtc agaggatgttgc cccgcctgtcc 780
 ctggatgtat tatgttgcgttgc tggcgttgcgttgc ctcgttgcgttgc ctcgttgcgttgc 840
 tgctcggtgggg cctgttgcgttgc ggtgtcccttc ctaaaggatgttgc cccatgttgcgttgc 900
 agcccttccac tcccttcgttgc ggtgtcccttc ctcgttgcgttgc cccatgttgcgttgc 960
 cttcttcgttgc agaggatgttgc ccccttcgttgc cccatgttgcgttgc cccatgttgcgttgc 1020
 gaaaggatgttgc ccaaggatgttgc aaaaatgtcaga aaacgcaggatgttgc cccatgttgcgttgc 1080

4584

(2) INFORMATION ON SEO ID NO. 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

(2) INFORMATION ON SEQ ID NO. 121:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 742 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

ctcacttcg caccactgcg tgactctaaggc cgacgcacgc gcctactctc gcactgcaga 60
 cggggaaact gaggcccgag gcggccgggg tggggcagac ctcccgccga gcccggcc120
 ccgcggcccg ctgcggccgc ctggcccgat aagaagcacc cggggcgcgaa ggcgaaggcg180
 cacagcgggg ggccaggatcg gttcaacgcg cgcgtatggca gtcagcgcgc tggcaaqcg240
 cgtgtcgatc aagctgcgtt ctccatcgcg ggcggccggg ccagggggca gtcccggggg300
 gctgcagaag cggcaccgcg ggttcacccgt caagtatgtac cggcgggagc tgcaagcgcg360
 gctgtggatcg gagaatgttg atcgacggccg cttggggagg ctgtacccgcg gcatggaggc420
 agacatgccc gatgagatca acattgtatc attgtttggg tttagagatg aagaggaggag480
 aagccggaaa atccaggacg tccgtggaa atgtggaaa cctgtcgagg acttcatcca540
 ggatgtgtc gcaaatcttc aaggccctca caggcagcccc ggcttcggcc agccaadgccc600
 ctccacacgc ggcagctca gccccttca ggaccggccg cggactgtctc acccctgtacc660
 ctcttgact ctccctgcg cccggacgcg gcccacgtt ctttgttata agttgtat720
 aatggttctg taacaataaa aa 742

(2) INFORMATION ON SEQ ID NO. 122:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2330 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

gttttgacaa gttgtttaa taggaaatag acctgcgtgc ttcatagggt tcctcaacc 60
ccttcctcca gttttcttaa aatggatcttccatccgc ttccacccca aatacgac 120
taatgttt ttcgtttagc accgtctgttccatgtt cttatgttccaa gaaacttgc ttacagac 180
aagaatttt tcctcgacaa gaacctcaat ctttgcgttccatggatgttccatccgc 240
tttgcgttccaa cagaagatcg gagggttgcgttccatggatgttccatccgc 300
agggttgcgttccaa cagaagatcg ctttgcgttccatggatgttccatccgc 360
tgtcatagaaac agcaacttgc ttccacaaacgc ctccatccacgg acctgtgttgc ttatggatgttcc 420
aaggcgacag aacccgttgc tgagggttgc tggtgtgtcc gatggggaaa aggacaaagg 480
ccccggggct ttggacatagc acagggttgc aatgttgcgttccatggggaaa gaagagatgttcc 540
tcacagaaac aaagctttgt cacacagaaa tgatgttgcgttccatccgc 600
tcagggttccaa gttgcgttgc gatggatgttccatgggttccatccgc 660
ggaagcgttca gggccgttca gggacagcttca tgatgttccatgggttccatccgc 720
aatagatcaa cttccatgttgc gtccaggaaac tggtgtgtccac agctacttgcgttccatccgc 780
tttctggggg ctggaaaaaa acacaaatccatccgc gccgacagcttccatccgc 840
agatgttccatccgc aatcttccatccgc tgatgttgcgttccatggggaaa acatgttccatccgc 900
gcttacaaacc cagtggcccg gaaggccctcc ttccggggaaa ctgttgcgttccatccgc 960
tgtttcaaaaag caataccatttgcgttccatccgc 1020
ggggataact ctggatgttgc gtttgcgttccatccgc 1080
ttttttatgttgcgttccatccgc 1140
tatataatgttgcgttccatccgc 1200
tatataatgttgcgttccatccgc 1260
gctgttccccc aattccatccgc 1320
ttatgttccccc tccaaaatgttccatccgc 1380
taagggttgcata cttatgttgcgttccatccgc 1440
cccttcatccgc 1500
tttagggatgttgcgttccatccgc 1560
ccatgttccatccgc 1620
gccccgtatgttgcgttccatccgc 1680
ttttttatgttgcgttccatccgc 1740
cctaataatgttgcgttccatccgc 1800
ggatgttgcgttccatccgc 1860
aaaccatgttgcgttccatccgc 1920
atgttgcgttccatccgc 1980
cctaataatgttgcgttccatccgc 2040
gtaaaagatgttgcgttccatccgc 2100
ctggatgttgcgttccatccgc 2160
aaagggttgcgttccatccgc 2220
aaagaatgttgcgttccatccgc 2280
tttgcgttccatccgc 2330

(2) INFORMATION ON SEQ ID NO. 123:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1860 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

gaggcagttt	gagatcacca	gcatttcgt	ggatgtctgg	cacatccctgg	aattcgacta	60
tagcaggcgc	ccccaaaaaa	gcatcgccga	gttccatcgat	ggggatgcct	atgtggcgaa	120
gttaggttc	atggtgagca	ccgcgtgggg	aatgcggcc	aaggggagac	actccgttgaa	180
ggcagccggc	aaagagaagt	gctctacttt	cttctggcaa	ggccggcaact	ccaccgttgag	240
ttagaaaggcg	acgtccggcc	tgatggacgtt	ggatggccac	gaggaaaggg	ggggccagggt	300
ccagggttcc	caggaaaggaa	agccccctcg	tttcttcgaa	tgtttccagg	ggggggatgggt	360
ggtgtcactcg	ggggggccggg	aaggaggaaa	agaaaaatqtg	caaagtggat	ggcgccgtgt	420
ctgggtgtgt	ggaggggtgg	ccgttggaa	gaattttgtgt	qaatggggct	fgtactgtgt	480
caggcttgggg	tccagaactt	catgttgggt	gtttaaccgtt	aaacaaggccc	tcatcttactt	540
gtggcacggg	tgc当地ggcc	aggcccacac	qaaggggatgt	ggaaggacccg	ctgcccacaaa	600
gatcaaggaa	caatgttcccc	ttggaaaggcc	actggatcatgt	acgacaaag	tccataataaa	660
cgatgtgtgt	gaaggctccg	agggacttcgg	attttttggat	ggttttttttt	ggagagacag	720
gaaaggcttac	gatttgcattc	ttaaagatcc	ttggaaagtttt	aacttcggcc	cccgccgttt	780
catttttttt	agcttttttttt	gggtttttttc	tttttttttttt	tttttttttt	tttttttttt	840
cccccttttttt	tgatgttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	900
agcataatttt	cttgcgttttttt	atcaccacgt	tttttttttttt	tttttttttt	tttttttttt	960
cgagaaacaa	atcaactgtt	ccggccggat	tttttttttttt	tttttttttt	tttttttttt	1020
gggatgtgtgt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1080
ccttatccac	gcttttttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1140
cagagggggc	atcgtttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1200
cgtttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1260
caggccactt	ccgggggggtt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1320
tttcgtttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1380
gttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1440
tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1500
tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1560
tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1620
tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1680
tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1740
tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1800
tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttt	tttttttttt	1860

(2) INFORMATION ON SEQ ID NO. 124:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 807 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vi) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

(2) INFORMATION ON SEQ ID NO. 125:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 1932 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

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ccccgggtttt gggctggAAC tcgcgcgCTT agagAGCTG gtggaaAGCTG ctaaaaGGCG 60
aggggggggCTT ctggcgAGTT ccTCCCTcoAC ccTCCCCCac ccTTCTTCGc caaccGGCT 120
ttcagccccCTT atggcgATTC cAGCcATTGc tcgaCTGCTG ccACAGCCTG ttTtcAGGCC 180
caaaacaACCG cAGCCGCTGT TCCCAggATG tgatGATCCTG tataTATTCG atTTCTCTC 240
ggCTTcatACG cAGTTAAAGA gaaAAACAAA ATGTCGTCG ttTCCCTAGA accAAACAAA 300
ataggATTTG aaaaaAGAA tattTCGACG ATGAAAGATA ATCCGAAGTG gATGAGAGAA 360
aatgtACCTG aaaaATGCTG accAGCACCAC GGTtACCCCG tccACCTTCG aTTTCTTC 420
gaaaggCAGT atGCggggGA ATGATGCGT TTCTTGGAG ccAGAGAAA TAATGAGCTG 480
tatgcCTCTT taggCTTGC AGCCCCACCT GGTtCAAAAGG AAGCAGAGT GCAAGCAAG 540
cagcAgACAT gAACCTTAAG CACTGTTGTT TAATGCTCTT GAAAATAGTG tCTTCATG 600
ttttttAAAAA TCCAGCAAGT AGCTTGTGCT CAAAAGAAAT AGCTTGAATG TTGAAATAAT 660
agatTTAGTG GTTTTCCAA TGCAAAACATT CAAAATGAAT ACCAAAATTA AATTGGAACA 720
ttatgtGTGAT tagTTGAGG AGAATGGGAT ATTACACATA ATTATTTATA ATAGTAGAT 780
atcgtAGAAA tagTTGTTG ACCTGCAGG CCATCTCTG TAACCAAGT ATTACACAA 840
gaaaACACCC TCCCTCTCTT OTCGCAATTAC TATGGCAACT TAATGTTG TCGAGCTT 900
cattttAAAGA gagaAAAGAGA AATAACCTGT CTTCATCTTC TAATGTTGCT CATTAAATT 960
catggAAACAG AATATGTTAC TTTTGTATGC TATATACTG CGTTAAAAGA GTTCTTGAG 1020
gtAAATGTTA TGTATGTTA ACCTGTGTAAC TTTCTTATGCA TTTTAAAC ATTCCTCAT 1080
tttttgtagAT gaaACTTCTT CATACTGAGC CACAGATTT CTGAGCTCTT AAATGAGCC 1140
tttcattGCA cATTTCAGTG ATCGAAATAG ATATCCTTTT ACACGCAAA AAGCAATAGA 1200
ttcacTTCTGT ggACACAGTC CTGTTTAAC TACACAGTG TGTGGAAAT ATATACCA 1260
ttGCTCTTGC TCGTAAGAT ATACATGATC ATATCATGA AGTGGGTGTC CAAGTAAGT 1320
taaaATGGCA TCTCTAGCA AAGAGATTAG ACTTTAAAT AACTTCTTAA TAAACAGGGTG 1380
ggcgtCATTT GCTTCCCTTG CCAAGAGT GTTTCCCTTG AGTTTGTCT AACTAAGAT 1440
ttccGGCTTTA AACAACTGCA ATCGTGAATA TGCTACTT CCTAAGATAT CTTACCTTT 1500
tatttCAGTT tagCCCTGTA TTGTATGAGT GTTATGCTG AACAGCTGG ATACTTTCTT 1560
atgcCTCTAT TCCAGCAAAA AGTAGAATG TCAAAATAAA AGGGCAACTT TAAAAATAT 1620
aagcCTGAAG ACTTCTAAA AGAACAGAAA CATGGCTAA ATAAACCAAA TAGATTCA 1680
tagtaAGTTT CACACTACCT TATTTCAAAAG ACCAACAAACCC TCTTACTTA AACTACCAT 1740
ttcgtATTTAT TCTTGTGTT CGTCGCTTCA CTTTGGCA AAATCACAT ATAAATGAGA 1800
gtgcCTTTG TTTCTAGA TCCAAACTTG ATGCTATGCT TTTAAATAAA CTCAGTACTT 1860
tttagAAACAT AAAAAGAAAAA AAAAAGAGC GACCCCCCGA GTAGTGGGEC CGCCGCCGG 1920
gatTTTCCG gg 1932

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(2) INFORMATION ON SEQ ID NO. 126:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 3024 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

(3) INFORMATION ON SEO ID NO. 127:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

(2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

PPLRLRLFFFY LRKFISTSTA EIRKWKYRFGQ IILYEMDPHT TSFLIQARYN IIPGFSKSSQ 60
 HGYLCYSVLA FIAASSFRRA FFSKFKLVKV SCLWAAFLPS ITMKMHPTTV RAIIR 115

(2) INFORMATION ON SEQ ID NO. 129:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

VROGAPGLSC GFVNQNPFILE KSELLVSLRD EETSLSHNLK QLPAARRRPL RLPMATCYSA60
 DQRRTSPGTW ALVSSMSPSV GV 82

(2) INFORMATION ON SEQ ID NO. 131:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

GIITLSLLMI IHPQMEEFIR QPLQFRLKTG AHRTQGTIKE DQEPRFFLSK NWP

53

(2) INFORMATION ON SEQ ID NO. 132:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

LFILRWRSL S VSHFSFVLKQ EPTGPKE L RTRNLGFFFQ KIGPSPINEG KN

52

(2) INFORMATION ON SEQ ID NO. 133:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

KKKPRFLVLL NSSLGPVGSC FTKKLKW LTD KLLHLMNNH Q

41

(2) INFORMATION ON SEQ ID NO. 134:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

ADPAFSTDLF QGCTDMAAAF RKAAKSRQRE HRERSSDYRK KQEYLKALRK KALEKNPDEF 60
 YYKMTRVKLQ GGVHIIKETK EEVTPEQQLKL MRTSGRQIYR KGRCRS 107

(2) INFORMATION ON SEQ ID NO. 135:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

RIRRSPFLS KAVQTWRRLF GRRLSPGSGN TESEAVTTVK NKNTSKLFGR RLLKKIQMNS 60
 TTK 63

(2) INFORMATION ON SEQ ID NO. 136:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes
 (vi) ORIGIN
 (A) ORGANISM: HUMAN
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:
 LFWGYYFFLSL LNNMYSTLEF NPSHEVVVEFI WIFFKSLLPK SFEVFLFFTIV VTASLSVFPL60
 PGLSRLPKSR RHVCTALEKI SGERRIR 87

(2) INFORMATION ON SEQ ID NO. 137:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

EANNYMSCQG GSRFHFSFIL PQYPGINAAT GGQSLFVLLP TPSLFCLFNS VKLFCLGPGK60
 EPKENLSGQV HFVNAENILK ARFLEYSQLA FFPLI 95

(2) INFORMATION ON SEQ ID NO. 138:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

NSSASSPQFW PNSRLAVFTW YPGVGLTLI SMMFSKMKLD KVDHQLHRVF CKSIVSKWPR60
 DLRKIQIFCL PWSCFKS 77

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

DLKQDGKQK ICIFILKSLGH LLTILLQKTR CSWWSTLSSF ILENIIIEIKV SNPTPGYQVK 60
 TASLLLGQNC GLLAEFLFYGL QSKWSYLTHH MTKVNLNRG KVNLNIQFWIQ EIIIVNFPPK120
 SMERMLVENI LKI 133

(2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 783 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

FLLQPSAFHL YEPLDVTMT WRMGPRTML LAMWLVCGE PHPHATIRGS HGGRKVPLVS 60
 PDSSRPARFL RHTGRSRGIE RSTLEEPNLQ PLQRRLRSVPV LRLARPTEPP ARSDINGAAV120
 RPEORPAARG SPREMIROEG SSARSRLRFE PSGSSSPNIL ASFAGKNRVW VISAPHASEG180
 YYRLMMSLLK DDVYCELAER HIQQIVLFHQ AGEZEGGKVRR ITSEGQILEQ PLDPSLIPKL240
 MSFLKLEKGK FGMVLLKKTL QVEERYPPV RLEAMYEVID QGFIRRRIEKI RQKGFVQKCK300
 ASGVEGQVVA EGNDGGGGAG RPSLGSEKKK EDPRRAQVPP TRSERVKVL KLAATAPALP360
 QPPSTRPRATT LPPAPATTWT RSTSRAVTA ARPNMTTAFFP TTQRPWTSP SHRPTTTEV420
 ITARRPSVNE NYLPPSRKDQ HRERPQTTRR PSKATSLESF TNAPPTTISE PSTRAAGPGR480
 FRDNRMMDRE HGRHDPNVVP GPPPKPAKEKP PKKKAQDKIL SNEYEEKYDL SRPTASQLED540
 ELQGVNPVLK KAKESKKHKEK LEPEKEKKK KMKNENADKL LKSEKQMKKS EKKSKQKEK600
 SKKKGGKTE QDGYQKPTNK HFTQSPKKSV ADLGSFEGK RRLLLITAPK AENNMYVQQR660
 DEYLESFCKM ATRKISVITI FGPVNNSTMK IDHFQLDNEK PMRVRVDDDEL VDQLRISLER720
 KEYGMYTNDF FMVLTVDVLR VKQYYEVPI MKSVEFDLIDT FQSRIKDMEN QKRGVFFEGG780
 KTP 783

(2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

KMVGVWVFL RWERMCENLF QGNGFAAEVR MCSCIDLQTP RRWVHTACLG VPRDSRPPTY60
 LSEARAAGHG PSAKPVCDAL GALVQEА 87

(2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

SFSSLGVRNT LFITFKFALY FFSSMLVLWT FGDVSVRAGE RGVRPSPHRW SWPPPSSL60
 PDHREFPICPS ENLSQGELKF TGQGTSFIYF IMLANRT 97

(2) INFORMATION ON SEQ ID NO. 146:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

ASCTKAPRAS HTGLAEGPWP AARASDKYVG GLESLGTPKH AVCTHLLGVC RSIQEHLTS60
 AANPFPNKRF SHILSHLKKT HTPTTIF 87

(2) INFORMATION ON SEQ ID NO. 147:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 119 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

NSKDKCFSLA FITTPETERW RCCASEPRLL ALKHQGHRTQ AWQRGHGQRH ELQTSMLEV 60
 NPLAPPMSMCQ APTFWVSADR YRNTSLPLQR THFPGKDFHT SSPTSKKPTh PQPFFKAPR 119

(2) INFORMATION ON SEQ ID NO. 148:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 87 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

STKGIAHRLG RGAMASGTSE RQVCWRSRIP WHPQACSVHP PSGCLQIDTG THPYLCSEPI60
 SLEKIFTHPL PPQKNPHTHN HFLKPHG 87

(2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

DPPSHSQLGR CCHRMVFESV GARAHFQLSQ QLGWHLPSA RNSNIMNARD SVLSKVFHPK60
GAGHGCRL 69

(2) INFORMATION ON SEQ ID NO. 150:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

SAHLGLPKCW DYRREHPCPA PFGWKTLST LSLAFIMLLF LALGSKCHPS CCDNQKCALA60
PTLSNTIR 68

(2) INFORMATION ON SEQ ID NO. 151:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

HHTQPIEVFL VATGFHHVGQQ AGLEPLTSGD PPTLASQSAG ITGVSTRALP LLDGRLY 57

(2) INFORMATION ON SEQ ID NO. 152:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 57 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

SAGIPKLAPK IPLPFS DLLK CYLISGAFFD HTLKTSTPTH GPCPPSRLHF LAYTYQM 57

(2) INFORMATION ON SEQ ID NO. 153:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 32 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

LKTLLTVASI RVSTFYSSDP TSFNLLLLIY GG

(2) INFORMATION ON SEQ ID NO. 154:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

TKRAVMKSMH LCAIRAFLVP HSELIDSODYI HF

32

(2) INFORMATION ON SEQ ID NO. 155:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

GRVRAVKGRH SDRSHSQQCF QSVNTDEVPT T

31

(2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

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(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

VQNVMMSACNF IFIKAKLIYM EYCSIYYAPI YILSPVVRYF ISLLLNIFYT YL

52

(2) INFORMATION ON SEQ ID NO. 157:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 59 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGTECFFFICC IENSHTQFSI LCQCSHHGWT LGRNSPQPFL VSFSQFFSVS RWAPVINLP 59

(2) INFORMATION ON SEQ ID NO. 158:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 38 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

LSLCPCWPGN FFQWCLLEEV FSSGQFKEIK LGNGEGGR

38

(2) INFORMATION ON SEQ ID NO. 159:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

GSILDMMQEI SSWSQKFPRG AVFLRNGVYL NNS

33

(2) INFORMATION ON SEQ ID NO. 160:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

KKLPQQGHHK LNYYLNKLHF LKIQHLLGTF DSRKRFPASY PKCF

44

(2) INFORMATION ON SEQ ID NO. 161:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 225 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

AAGGLGLGVG PRGMWRAGSM SAEIYGVCAL RAVNERVQQAA VARRPRDLPA IQPRLVAVSK 60
 TKPADMVIEWA YGHGQRTFGE NYVQELLEKA SNEKILSCLG EIKWHPIGHL QKQNVNKLMA120
 VPNLFLMLETV DSVKLADKVN SSWQRKGSPE RLKVMVQINT SGEESKHGLP PSETIAIVEH180
 INAKCPNLEF VGLMTIGSG HDLSQGPNPD FQLLLSLPEE TVVKS 225

(2) INFORMATION ON SEQ ID NO. 162:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 99 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

CRGPGARRRS PGDVESWQHV GRAGSRVRIA GGERARAAGC GAAAAGSPSH PAPASGGQQN60
 QTCRHDGRGL WTWAAHFWRE LRGSTARKSI KSQNSVFVS 99

(2) INFORMATION ON SEQ ID NO. 163:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 120 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

LRSCPCKLPMV ISPTNTSRLGH LAFMCSTMAM VSEGGRPCLL SSPLVLIWTI TFNLSGEFPFL 60
 CQEFLFTLSAN FTTESTVSSMK RLGTAINLLT FCFCRWPMPKC HLISGHKDRI LGFDAFSSSS120

(2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

TSTGPSSPLV ASAATELAAF AAAFSSACMR PEGSASLEWN RLPLLMFGDL QGCEAREGIA60
 MRILQASFSG LSSKG 75

(2) INFORMATION ON SEQ ID NO. 165:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

NTHGDALTCL TPLQVPKHEE GKAIPKQRGR TFRAGTCRAK GSGKSCQFSC SRGYQGAGGT60
 SAGLALYLHT RTAASRGTSQ SPVGSVAPQQ 90

(2) INFORMATION ON SEQ ID NO. 166:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

SHPFEDSPEK EACKIRMAMP SRASHPCRSP NMRRGRRFQN REAEPSGRIH AELKAAAKAA60
SSVAAEATRG LEGPVLV 77

(2) INFORMATION ON SEQ ID NO. 167:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 347 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

TAFPLPVVVA AVLWGAAAPTR GLIRATS DHN ASMDFA DLPA LFGATLSQEG LQGF LV EAHP 60
DNACSPIAPP PPAPVNGSVF IALLRRFD CN FDLKV LNAQK AGYGA AVVHN VNSNELLNNV 120

WNSEEIQQQI WIPSPVFIGER SSEYL RALFV YEK GAR VLLV PDNTFPLGYY LIPFTGIVGL 180
LVL AMGAVMI ARCI QHR KRL QRNR LTKEQ L KOI PTHD YQK GDQYDVCAIC LDEYE DGDKL 240
RVLPCA HAYH SRCV DPWLTQ TRKTC PICKQ PVH RGPGDED QEEET QGQEE GDEGE PRDH P 300
ASERTPLLGS SPTLPTSF GS LAPA PLV FFG PSTDPPLS PP SSPV ILV 347

(2) INFORMATION ON SEQ ID NO. 168:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 588 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

QVTNMSDKSE LKAEELERKKQ RLAQIREEKK RKEEERKKKE TDQKKEAVAP VQEESDLEKK 60
 RREAEALLQS MGLTPESPIV PPPMSSSKS VSTPSEAGSQ DSGDGAVGSR RGPIKLGMAK120
 ITOVDPRE IVTYTKETQT PVMAQPKDE EDDDVWVAKP PPIEPEEEKT LKKDEENDSK180
 APPHELTEE KQQILHSEEF LSFFDHSTRI VERALSEQIN IFFDYSGRDL EDKEGEIQAG240
 AKLSLNRQFF DERWSXHRVV SCLDWQSQYP ELLVASYNNN EDAPHEPDGV ALVWNMKYKK300
 TPEYVFHCQ SAVMSATFAK FHPNLVGGT YSGQIVLWDN RSNKRTPVQR TPLSAAAHTH360
 PVYCVNVVGT QNAHNLIISIS TDKKICSWSL DMLSHPQDSN ELVHKQSKAV AVTSMSFPVG420
 DVNNFVVGSE EGSVYTACRH GSKAGISEMF EGHQGPITGI HCHAAVGAVD FSHLFVTSSF480
 DWTVKLWTTK NNKPFLYSFED NADYYVDVMW SPTHPALFAC VDGMGRLLDW NLNNNDTEVPT540
 ASISVEGNPA LNRVRWTHSG RGGCGGILK DKFCYFAMLG GAVCWSPQ 588

(2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

FHVEQLSHSF LSWRKDTIQR GSKDFVKRGI HNLLWSKCPH L

41

(2) INFORMATION ON SEQ ID NO. 170:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

CPRDVGTCSI VNYGCHVLQN PYCPFELCPS SKIRSYDSIV QHGIIMKSLS SSIFP

55

(2) INFORMATION ON SEQ ID NO. 171:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

KAFLVLSFPK WALFLVIHMT LFGCGCLLNF LEWTSFSKPK PARDRKGNGN

50

TRANSLATED FROM PDB

(2) INFORMATION ON SEQ ID NO. 172:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

CTFNIESFIY LIVYRTFHNY THLLHNILTS IKKFFCTSSF SFNLVKPVIH TNVYCELSEG60

(2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

EESFVFLIHS FVNRYKGTVN LTYTKKKIL VYPLMLIHRV LSYNVIQLGS LTFFPKNIFI60
 EKGITLS 67

(2) INFORMATION ON SEQ ID NO. 174:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 56 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

LYHIIRKHSV DQHKWVHKNF FFLGVCKHIC SFISVYKTVN QKDKTFFLVE VIFFLN 56

(2) INFORMATION ON SEQ ID NO. 181:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 289 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

SRRRTQGAASL RFPQPDTIGQ DFSASAQRGG LVAHSDLDER AIEALKEFNE DGALAVLQQF 60
 KDSDSLHVNQK KSAFLCGVMK TYRQREKQGT KVADSSKGPD EAKIKALLER TGYTLDVTG120
 QRKYGGFPFD SVYSGQQPSV GTEIFVVGKIP RDLFEDELVP LFEEKAGPIWD LRLLMMDPLTG180
 LNRYGYAFVTF CTKEAAQEAIV KLYNNHEIRS GKHHIGVCISV ANNRRLFVGSI PKSKTKEQIL240
 EEFSKVTEGL TDVILYHQPD DKKKNRGFCF LEYEDHKTAA QARRRLIEW 289

(2) INFORMATION ON SEQ ID NO. 182:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

KLCTEWLKVG GIWRWMRGSC LGRLCFTWIR VGLREEIGV

39

(2) INFORMATION ON SEQ ID NO. 183:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

EAVMTLILIL HTYFLTQPYS NPSEAKPSQT APSHPSPYPP NL

42

(2) INFORMATION ON SEQ ID NO. 184:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

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(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

PSFSFYTPIS SRNPTLIQVK QSLPRQLPLI HLHIPPTFNH SVHNFYSLHT SYLLIFLTNK60

(2) INFORMATION ON SEQ ID NO. 188:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 46 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

RSRFHMMMLTL RALQLSLPTK IGGACFRVSR LSPTEKKKKK MSLEEA

46

(2) INFORMATION ON SEQ ID NO. 189:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 65 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ITFSHDAAQ GASIIIPPHKD RWRRVFQGLSS LSYRKKEKN VIRRGVTRQS VPRFVFPGVA60
 ERDQF 65

(2) INFORMATION ON SEQ ID NO. 190:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 66 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

ECREAGPLFL QSRLELISFG HSRKHKGDG LTCYASSNDI FFFFFSVGER RETLKHA^{PI}₆₀
 FVGRDN ⁶⁶

EXCEDED BY THE SEQUENCE

(2) INFORMATION ON SEQ ID NO. 191:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 48 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

RQTEGETEML RKPSYTTLPR NTSLRECKKY YWRWKSRSKTA MGRRPRGD

48

(2) INFORMATION ON SEQ ID NO. 192:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 60 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

RAETRSQGQL NEDKLKGKLR CLESPAIQLY PEILPLGNVK STTGDGRAEK QLWAEGQQVI60

(2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 44 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

SCIAGLSKHL SFPFSLSSLS CPWLRLVSALQ LLPLRCAFPPA SDLL

44

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 98 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

EIMNGLVLNDN IWPHKLLTSV LGESHFVNHT SEIYMMNLGE QRRSCCKRCI KYLCCFCMRL60
 RSFSHLSPLF PIRISREAKL FCGFGNGHFP GKCIWIDD 98

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

AHSSTKAASK SEFLLILPLC NTLRSSHNCP TPHLPVSCCT KSPSLSSFRY IVRQGRALR 60
 RRAFEALSTL PASVKMRLHY SPEKRARFSH RSRCIFPGND HSQTHRTVWL LWISL 115

(2) INFORMATION ON SEQ ID NO. 196:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

SGVKRISCVL ETKAYCHCFK KSLCEMKKNM TNTGSHTYTY IQRNLHTCTH TGRYRHTVPP 60
 KRSNPNQSSYR FYHSVILSEV PTTAQHLYTP FPAAQSLLHS HLFDTSSGRA EGHYAAEHSR120
 LSAHCQPA 128

(2) INFORMATION ON SEQ ID NO. 200:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

RPGVVEPPLLR RLPDSETQKR VQGWGEMWSE GRFAFEKGSS RTHWDIVTHL NHLLIERCWP60
PNNGRSGPGP RA 72

(2) INFORMATION ON SEQ ID NO. 201:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 77 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

GPSPYARGPG PDLPLLGQQH LSIRRWFKCW TMSQCVLLELP FSNANLPSLH ISPHPWTRFC60
VSESGNLLKR GGSTPGL 77

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 60 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

EANTFLSEDG SNVLQCPSVF SNFLSQMQTF PHSTSLPIPG PVSVSLSQAT FSKEGVPLPA60

(2) INFORMATION ON SEQ ID NO. 203:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

PTTTLVPLF FLSSRKRKQK DSFQTALCSL HCSFPKQAAS TGKAHVVT PY FSEVLLFHGV60
 TLLSESKFRK QVLPLADKNH TSFL 84

(2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CDRVPLEFLSY WCAVADSWLT ASSVSHVKGI LSPQPTECAP PGPANCFFNE FFFFFFFLVET 60
 GGSFVVAQDGL ELLGSSNPFT LASQS AETIG MSHYAQPEQD DLNLINSTPK QQQLSLSQGCQ120
 GGLCEGRKD 128

(2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

WVAGRRHLLS VQTKSLQVLG LDLCTVPESQ CIRLYKKLV WFLSAKGKTC FLNLLSDNKV60
 TPWKRRTSEK YGVTTFWFPV LAACFGKLQC RLQRRAV 96

(2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

PDFRGFAGFA MFSRGFQVGR GERQGENAPC RGVQRSPASC PAVGWTSDL

49

(2) INFORMATION ON SEQ ID NO. 207:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

QISGVLRAPR CFPEVFKEE ESDKVKMPRA GASSGVLPBV RRWGGRLLIYE GAHPPI

56

(2) INFORMATION ON SEQ ID NO. 208:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CCSCQSSQVR YSDRWMGTFI NQTSTPPPDS WQDSAGRPGT GHFHLVALLF PLENLWKTSR60
GPQNPGNL 68

(2) INFORMATION ON SEQ ID NO. 209:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

WGGRRTLASAV SIPLRKCHSH RPTVLARKQP QSGVPPPYTA IASPDASGIP VINCRVCQSL 60
INLDGKLHQH VVKCTVCNEA TPINKPPTGK KYVRCPCNCL LICKDTSRR1 GCPRPNCRRI120
INLGPVMLIS EGTTSSACIA QSQPEGYKGR VLGHGWGTHS LWDG 164

(2) INFORMATION ON SEQ ID NO. 210:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 218 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

SSAVPDGAVG RPVAVAVGGP PHSCRCPCC LMRAIGVHLG CTSACVAVYK DGRAGVVAND 60
 AGDRVTPAVV AYSNEEIVG LAAKQSRIRN ISNTVMKVQ ILGRSSSDPQ AQKYIAESKC120
 LVIEKNGKLR YEIDTGEETK FVNPEDVARL IFSKMKTAEH SVLGSANDV VITVPFDGE180
 KQKNALGEAA RAAGFNVRL IHEPSAALLA YVGQDQSP 218

(2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 186 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

RKWTLTSMSQ KRMLKRPDNK LKYVTKWQRT AKQITHPFSR NSTMSSMNIT ILTSPTSSRK 60
 YKRAEERRIV RMGESMKTYA EVDRQVIPII GKCLDGIVKA AESIDQKNDS QLVIEAYKSG120
 FEPPGDIEFE DYTQPMKRTV SDNSLSNSRG EGKPDLKFGG KSKGKLWPFI KKNKLMSSLT180
 GGPFST 186

(2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

ISGRRVSLNF VSEFSITEFC PCWCLGYRPD GPGSFPSCSG LEVSPLHFLK ACVQCSPKSI60

(2) INFORMATION ON SEQ ID NO. 213:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 68 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

DLCSTTLSATK GSITCFLNKA LVSPPASSGL HYSETNSTSF AGGITVPISR LGPALQTSFG60
LLVLLTLL 68

(2) INFORMATION ON SEQ ID NO. 214:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 54 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TISFFKSKRG LKQEGTGTTSS QMDLGEHCTQ ALRKCKGLTS RPEQDGKLPG PSGL

(2) INFORMATION ON SEQ ID NO. 215:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

LPTAFLSSV FWIEMTWIL FFPDLAGAPF YFSFIFSIVA FLYFFYKTWA TDPGFTKASE 60
 EEKVNITL AETGSLDFRT FCTSLIRKP LRSLHCVCN CCVARYDQHC LWTGRCIGFGI20
 NHYYIIFELF FLSMVCGWII YGSFIYLSHH CATTFKEDGL WTYLNQIVAC SPWVLYIIML180
 ATFHFSWSTF LLNNQLFQIA FLGLTSHERI SLQKQSKHMK QTLSLRKTPY NLGFMQNLD240
 FFQCGCFGLV KFCVVDWTSQ YTMFHFARE KVLSRV 276

(2) INFORMATION ON SEQ ID NO. 216:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

SPSRSPVVFA GEFLFKHPFV EESLMSFFHP DLHLMNPKAI STQFLYSVF

49

(2) INFORMATION ON SEQ ID NO. 217:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

KEINNYIRKE KNFKYLDQPST PNHPQDRWVQ KNAFWFY

37

(2) INFORMATION ON SEQ ID NO. 218:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

KFSSKDDRTS RRRSIIISER KKILSIYNPL LLITPKIGGS RKMHLGFTEE RS

52

(2) INFORMATION ON SEQ ID NO. 219:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

DKRNGIISKK LSPEKTTLKS ILKRKGTSOI SOESODDIEIS SKSRVRKRAS SLRFKRIKET 60
 KKELHNSPKT MNKTNQVYAA NEDHNSQFID DYSSSDESLS VSHFSFSKQS HRPRTIRDRT120
 SFSSKLPSHN KKNSTFIPRK PMKCSNEESC 150

(2) INFORMATION ON SEQ ID NO. 220:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 83 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

NKWNKSKLGK EISKATQSLD PAQLADPCHS LAVAASLCSL KGEPGQCFFPS PWANSLHSGK60
 QTSGPFPKSQ ECLAAWWVLI AMF 83

(2) INFORMATION ON SEQ ID NO. 221:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 83 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

NSKLVDCRMETWLLRHWSF SLCVSCWGVV MIVSALTHCT RWQQDTALHK MAAPLQLPPQ60
 PPSLHPHRFG LWFLSSVTYC LRS 83

(2) INFORMATION ON SEQ ID NO. 222:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 90 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CLHNREPDIF RILSSYYGI LRPRSYLQTK WFWSLQNIAM STHQAARHSW DLGKGPLVCF60
PLCSDQAQGL GKHWPGSPFS EHREAATARE 90

(2) INFORMATION ON SEQ ID NO. 223:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

QSLRHCLWNI SLQRDGAFKE PGAGPVSSKA LDVFLVRTRR GCQMPLKPSG LVWPRAAGQG 60
RAEKWSSSQL ALPSPTQPRP RWSDLTSILTS ASPKVQMSKC LVVQSQEMGS YLKs 114

(2) INFORMATION ON SEQ ID NO. 224:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 145 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GCVGGGRAEAE MAEKFDHLEE HLEKTVENIR QLGIIVSDFQ PSSQAGLNQK LNFIVTGLQD 60
IDKCRQLHD ITVPLEVFEY IDQGRNPQLY TKECLERALA KNEQVKGKID TMKKFKSLLI120
QELSKVFPED MAKYRSIRGE DHPPS 145

(2) INFORMATION ON SEQ ID NO. 225:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GQTMRTEGLR GVSRAQS HLS RKVASALAVP ASRRIAVPGD LHTGRVSWLR RRVILPPDAS60
 ILSHVFRKYF RKFLNQQAFK FLHGVDLAFN LLIFS 95

(2) INFORMATION ON SEQ ID NO. 226:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

ALRPPLYALG QQVGAUTGPA DCSATAPLDF WIFWKQS QNS GLLGGWQRGM VRGPPFISLF60
 SIRWQSTGH P WWWSGPRPMP TLFFESR 87

(2) INFORMATION ON SEQ ID NO. 227:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

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(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

APALATQPPL SLPRGTGPAY LNSLTLMLQT WLLOSKLLSS NVLLPHFHFL HICLLLYWEL60
 LLNLNFHHSWA LCLPFFSA 79

(2) INFORMATION ON SEQ ID NO. 228:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 87 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

RSMSVEASEV CLGTTGRCCCH WSCRLFSNSP FGFLDILETK SEQWPTGGLA EGYGKRTSFH60
 LPVQHPMAHV RSSLVGVRPK THAHHTL 87

(2) INFORMATION ON SEQ ID NO. 229:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 150 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATLSRFFGRI FNRLRLTQVFPLFLFSSPNOKK SFCSIEGEWN GVMYAKYATG ENTVFVDTKK 60
 LPIIKKKVRK LEDQNEYESR SLWKDVTFNL KIRDIDAATE AKHRLEERQR AEARERKEKE120
 IQWETRLFHE DGECWVYDEP LLKRLGAAKH 150

(2) INFORMATION ON SEQ ID NO. 233:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 206 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

DSLRRGLGIC LWEFIHLSLL FTSPKPGFPF LKPAVISQLE GGSELGGSSP LAAGTGLQGS 60
 QTDIQTDNLD TKEMYEGKEN VSFELQRDFS QETDFSEASL LEKQQEVHSA GNIKKEKSNT120
 IDGTVKDETS PVEECCFSQS SNSYQCHTIT GEQPSSGCTGL GKSISFDTKL VKHEIINSEE180
 RPFKCEELVE PFRCDSQLIQ PSREQH 206

(2) INFORMATION ON SEQ ID NO. 237:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

RIRRSALIFS KGVQRWRRVF GRRVSPGSGN TESEASDYRK KQGTSKVFGF RVLKKIQ 57

(2) INFORMATION ON SEQ ID NO. 238:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

GTLFFTVVTG FALCVPAAGT YPPSENPPPS LYTLGKDQCR TPDP

44

(2) INFORMATION ON SEQ ID NO. 239:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 74 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

NLYPTLEFNP SHEVVELTGF FSTPFFRTPL RYLVFYGSHW LRSLCSRCD LPAFRKPAAI60
SVHFWKRSVQ NAGS

74

(2) INFORMATION ON SEQ ID NO. 243:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 183 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

AAVAFGAKGT SPAEARSSRG IEEAGPRAHG RAGREPREERRR SRQQRGGGLQ ARRSTLLKTC 60
ARARATAPGA MKMVAPWTRF YSNSCCLCH VRGTILLGV WYLIINAVVL LILLLSALADP120
DQYNFSSSEL GGDfefMDDA NMCIAlAISL LMILICAMAT YGAYKQRAAG SSHSSVTRSL180
TLP

183

(2) INFORMATION ON SEQ ID NO. 244:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 157 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

CQHVHCHCDF SSHDPDMCYG YLRSVQATRS WIIPFFCYQI FDFALNMLVA ITVLIYPNSI 60
 QEYIRQLFPN FPYRDDMSV NPTCLVLIL LFISIILTFK GYLISCVWNC YRYINGRNSS120
 DVLVYVTSND TTVLLPPYDD ATVNGAKEP PPPYVSA 157

(2) INFORMATION ON SEQ ID NO. 251:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 81 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

ATKTVPRQRW SPPHCPRPNP SLNLLRCGWG NRGKTEAPDA FSLLCSSAID CPDVQRETHT60
 RFAHENWGAD GQADRLCLFS E 61

(2) INFORMATION ON SEQ ID NO. 252:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 97 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GVDGETAEKL RHLMHSAACCA AVPLTALMFR EKRTQGLPMR IGEQMAKQIG YVCFLSDEVR60
KPCGSGGHHLW FILFFPYPWLL EMVTFRTVQL HLSEHYC 97

(2) INFORMATION ON SEQ ID NO. 253:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

LEILGIFSRV SKLSSSPTDT HPSSQIGVAI LGGRVVYGT P GCLHISQNYP RTIVPKSRVF 60
TGRQNLFSMP VPQLLSQIPI LGSHQLPIPH QTATVPSLSP YCSFKSCSQE RNCH 114

(2) INFORMATION ON SEQ ID NO. 254:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 53 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

IPSPQGPFCR SYSDPRKCPF PIVVLCNWGL VYPRGNCGEI IGLRVKRALV LEL

(2) INFORMATION ON SEQ ID NO. 255:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

QVDTIISTRK GLKLQNQCSL DSQTNDFSTV TPGID

35

(2) INFORMATION ON SEQ ID NO. 256:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TKPQRHRTTM GKGHFLGSEY DLQNGPCGLC IYPYAVPWSN A

41

(2) INFORMATION ON SEQ ID NO. 260:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 205 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

TRANSLATED

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

GSVKVPASPR PGGTSLLGPV AAKELSFSRP NGRRGQLPRP PGSLTLLLFF SSPASRGPA 60
 LSPGGIRLLL PPPPHLLPGQ PACPAAVMCD KEFMWALKNG DLDEVKDYVA KGEDVNRTLE120
 GGRKPLHYAA DCGQLEILEF LLLKGADINA PDKHHITPLL SAVYEGHVSC VKLLLSKGAD180
 KTVKGPDGLT AFEATDNQAI KALLQ 205

(2) INFORMATION ON SEQ ID NO. 264:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 180 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

RNMSSFSRAP QQWATFARIW YLLDGKMQPQ GKLAAMASIR LQGLHKPVYH ALSDCGDHVV 60
 IMNTRHIAFS GNKWEQKVYS SHTGYPGGFR QVTAQQLHLR DVAIVKLAI YGMLPKNLHR120
 RTMMERLHLF PDEYIPEDIL KNLVEELPQP RKIPKRLDEY TQEIIDAFPR LWTFPEDYRL180

(2) INFORMATION ON SEQ ID NO. 265:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 78 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

VIGYGPSRINS EPSPVIYNRP GNNVKLNCMA MGISKADITW ELTDKSHLKA GVQARLYGNR60
 FLQPQGSMTH SACHKEGW 78

(2) INFORMATION ON SEQ ID NO. 266:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

ATPLCGMLNG SLIPGVVEEIC FHTDEPEPLP SDATYPLTPT

40

(2) INFORMATION ON SEQ ID NO. 267:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

VGIWQEDHLP QSLGFLNKKKE IVFLSWLLRL LKLALPLKYD ISFAVNLKL VASSVAHFQF 60
 LYQASLLSFP LRMGQVCSGG HSVRFSRGFG RGFKGKYSGG RMGSGVKVGD KGGRAKGGVE120
 GWGPYLDRGM PGGQGK 126

(2) INFORMATION ON SEQ ID NO. 268:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

LVYPKQGTKE PGKRSGHVKR DTQDTLIRDQS GSTPVLLPEC LCVNPCFLQN KRQQRKLLNQ60
 NTDPMRNGAC FCDPGELSAR LQELETGQLL IF 92

(2) INFORMATION ON SEQ ID NO. 269:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 103 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

NLVYTMWLQI YVN VHFEHIY VLWKEMLVTK IRFTLKEEEEF YSKHSNILFK CFKIQSIVFK 60
 VAVKASTYVK TQKEGSSDRN TAPLLCCFSC SLYTLSKHLL SGA 103

(2) INFORMATION ON SEQ ID NO. 270:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 82 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

FIYKQSKVRD IFAVTLAILS LQSPTSRVQC TSNNSLKTRH LTISVYLVCK VNKKSSIKE60
 LCFYQRSLPS EFLHKLMPSL QL 82

(2) INFORMATION ON SEQ ID NO. 274:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

QQHHLPQSLG FLNKKEVVF1 TWLLRLLKLA LPLKYDISFA VLNLKLVASS VPHFQFLYQA60
 SLLSFPIRMD MCCSACHVCN ASCREFGHSI KEKIQ 95

(2) INFORMATION ON SEQ ID NO. 275:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

LLHQYHTSSF YTKPVSSVFP LEWTCAVQRV MSVMLHAESL VIVLKRKYSE VTMSPE 56

(2) INFORMATION ON SEQ ID NO. 276:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

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(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

HAEQHMSILM GKLRRLAWYR NWKCGTDEAT NFKFRTAKLM SYFKGRANFN NLNNQVKNTT 60
 SFLLRNPND 69

(2) INFORMATION ON SEQ ID NO. 277:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 95 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

YILEIISBLKP SLAPTSGLM PQGFPPHFECN PRYPSLSTPS QTPTPGIARE DFGLANCVGY 60
 VSVVLIRDVH DCQSAFLTSV TTLLRCNSSQ KKTFS 95

(2) INFORMATION ON SEQ ID NO. 278:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 133 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

PTQFARPKSS RAIPGVGVWD GVDNEGYLGL QKWGGNPWGI SPQEVGASDG FRGDISNIYQ 60
 PWALSPCCSQ HGPHTSSLRL TWELVRNAGS PRSIELEAVL TRSPVIFMAQ SSFLDRCRCL 120
 LSAGMRHPWG RCG 133

(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

LKQHSHNQHN LLGOSLHGQS LGWESGMGWI MKDTWGCRSG VGIPGASVHR RWGPAMASGV 60
 LFPIYISPQGH SRPAAHSMVL TPAASALPGS LLEMQDLPDL LS 102

(2) INFORMATION ON SEQ ID NO. 283:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

VYSANEQQNF QFIDGYSAAD ESLCVSHFNF CKQRHRPRTV RGRTSFSSKL PRHNKENSTF60
 ISRKPMECNSN EEVVNQGGQSD GSMGKF 86

(2) INFORMATION ON SEQ ID NO. 284:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

GAEVLVFLQNC LGIIRKIAALL FQGNRWNVQM RKLLIKGSRM DQWVNFRWRQ GGAYIHSNPD60
 VIWSGQGWK 69

(2) INFORMATION ON SEQ ID NO. 285:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 59 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

LTTSSFEHSI GFLEIKVLFS LLCLGNFEEK LVLPLTVLGL CLCLQKLKWL THKLSSAAE 59

(2) INFORMATION ON SEQ ID NO. 286:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 65 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

GKEPQPESNS IMVKFPTESS CEWVIRKNED PKDKNQRQMG SVTGSLSIL NPIEYCGLT60
 CQGGD 65

(2) INFORMATION ON SEQ ID NO. 287:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

FLSFGSSFFL ITHSQDDSVG NLTMIELLSG WGSFPHRKDI LKTKKYLN

48

(2) INFORMATION ON SEQ ID NO. 288:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ARNIQSDLEW MIKIQSQTPS VFDFCLLDPH FS

32

(2) INFORMATION ON SEQ ID NO. 292:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CAKLETGDF LSYLFACAS PSNLVHLSSH SCYEQVKQDI LGVKSLWVFC FYVYKNGFCV60
 PFPCKYQLIW KLTIM 76

(2) INFORMATION ON SEQ ID NO. 293:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 63 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

VELSLLFPQL SQLLVNFKEA GHDDSHLLSQ NGRRRWADS LSPGVQDEPG QYGPTSSLTK60
 HPH 63

(2) INFORMATION ON SEQ ID NO. 294:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 73 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

PPKCLVSLEN NMNETKDEPD YLVTHRRRTS SSGNQILFQA WHIKGKKGSE RRVRKYHLKP60
 QKIWQRTASK SIR 73

(2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

PLGPASSAFG PSGSKSRSEE GRDGTAASPGT FKYHPWSPLS SLREWTSQST SSGLSDL LLC 60
 LYQPWQGSRI HLVGSGPSQY HWGSNKFLEP QSLGPGSQLI GDGVPPFQARA EFGTSGHELE120
 GNSVSYELGP WP 132

(2) INFORMATION ON SEQ ID NO. 299:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

ESRRGALAGP LSKAGEGRPG WYLNVPGMLS KPFPLPHSYSL TLMAKARDAG PKGKNVLSVF60
 SGFYSLVSLH 70

(2) INFORMATION ON SEQ ID NO. 300:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

GVKAREYRED VFTFRACVSG FGHQGQRVGV RKEGMGQHPW DVQVPSWSPF SSLREWTSQS 60
 TSSGLSDLLL CLYQFWQGSR IHLVGSGFSQ YHWGNSNKFL PQSLGPQLSQL IADGVPFKLV120
 PARAEFGTSL KGNSTVYELG PWP 143

(2) INFORMATION ON SEQ ID NO. 304:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 408 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

FANWEFMGTE QLQPQLPLPK VWSCRGCRQG PTKFNQVSRM QTAPAVSRRV GLAVSLTPPP 60
 SGQSGPSPVMG KAAACPAATPA SAPSQGLSFV GPVSCWPGSPP LLHLLIGGRQL LDLCPGCGRS120
 LPFSSSSSSS VSNDASAPDGP RGLGCFFGGVV LGGRGEKYLL YFLFVAATQQ ILLLGRASAF180

LKRDVGDPLV VAPAFFAVAG HLHQAVALPG VRVRVRDQET MQVSGLGGAL GLGRLSQELR240
 QALHARHFD VDVVVTAEGL DEREVDLQGD VILLLLVNGQ EAEDHAWVWH IHQLGRLVHP300
 HCEAILALSG HQKLLHRGGH RLHLLRRVVA RHELFQRHVA IIIHSGCGST AVPREKLQNP360
 SQRAQNLPTE LERSSKTFKG QRNPSRKGGK IYCKVVLGEDN PGSCGNQR 408

(2) INFORMATION ON SEQ ID NO. 305:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 169 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GWGVWQAGLD PVLGPPSSAV PSLLLGVVSM VWPFLQLCLS AVPLASSSLN SAAWSPVSSR 60
 ARQGWWGWCW QQLLSCDLS GLHLRGRRNGP GYRGQIHPGW SPRPPGLGAA GGRWLLVGRW120
 PSCLACLPCL SSSPNALSVS AFLAPGLSTP SAYKAVSPPQ TTVWLQPIR 169

(2) INFORMATION ON SEQ ID NO. 306:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

ILQLGHQFPL VPARAGAVGV GSSFSLGATF PASTSEVGGM QAIEVRFIQA GVLVLRRAWGL 60
 LGGAGCWEG GHRAWLVPFA SLLLLTLCLS LLSWPRAASPL PQIRLCLLL RPQSGSSPSG120

(2) INFORMATION ON SEQ ID NO. 307:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 472 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

SESLTHPGEE PGGPPPGGAP TMATPLVAGP AALRFAAAAS WQVVGRGCVE HFFRVLLEFLR 60
 SLRAVAPGLV RYRHHERLCM GLKAKVVEL ILQGRPWAQV LKALNHFFPE SGPIVRDPKA120
 TKQDLRKILE AQETFYQVKV QLSEAPVDA SKLQELEQYE GEFFLAAMEK LLFEYLQCLE180
 KALPTPQAAQ LQDVLSTMQP GVSIITSSLW RQYGVDMGWL LPECSVTDGV NLAEPMEQNP240
 FQQORLALHN PLPKAKPGTH LPQGPSSRTH PEPLAGRHFN LAPLGRRRVQ SQWASTRGHH300
 KERPTVMLFP FRNLGSPTQV ISKEPESEKEH AIYTADLAMG TRAASTGKSK SPCQTLGGRA360
 LKENPVVDLPA TEQKENCLDC YMDPLRLSLL PPRARKFVCP PSLCSSVITI GDLVLDSDDE420
 ENGGEGKES LENYQKTKFD TLIFTLCCEYL PPSGHGAIPV SSCDCRDSSR PL 472

(2) INFORMATION ON SEQ ID NO. 308:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

PGFALRGAIG PREGRGGGRG YRRSSGRQPL VSWQRQARCG SGGAMSFCSF FGGEVFQNHF 60
 EPGVYVCACK GYELFSSRSK YAHSSFPWF TETIHADSV A KRPEHNRSEA LKVSCGKCGN120
 GLGHEFLNDG PKPGQSRF 138

(2) INFORMATION ON SEQ ID NO. 309:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

SYGATAAFLS RSEASYFRTD CETGFRFLPS WTRGQGCAPS ACLPSRSQTI PTLAGLEGFD 60
 QSGSCSDQQQ GGWQGRPPFP FCILSSLGDV GLSFGEDESL SWNWASQGRV QRQGQEKKVR120
 V 121

(2) INFORMATION ON SEQ ID NO. 310:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 249 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

SEQGAKSADS VAAQPRPVPA EGMNHQQMSL FSKKRKGKLVQ SRGLGSVLMF QPLRPAFLSR 64
 RPFQFQLQQGM ANVWFQCQGR LGWVWAARLV TLGGRSFFAF RDKLQRRAEY SESGLPRLGA120
 VVQELVVAQPI ATLATGHLQG FRSIVLRTLGE HAVGVNGLGE RRPWRRVCIL RAAGEQPLIAT180
 LGTHVNARFK VILENLAPSEE AAERHGATGT AARPLPLETDQ RLPTRRPPVP ASTSPPLPRT240
 NRSPEGESR 249

(2) INFORMATION ON SEQ ID NO. 311:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 204 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

LGSSWIFVNL TVRFLCILGKE SFYDTFHTVA DMMYFCQMLA VVETINAAIG VTTSPVLPQL 60

IQLLGRNFIL FIIFGTMEEEM QNKAVVFFFVF YLWSAIEIFR YSFYMLTCID MDWKVLTWLR120
 YTLWIPLYPL GCLAEAVSVI QSIPIFNETG RFSFTLPYPV KIKVRFSFFL QIYLIMIFLG180
 LYINFRHLYK QRERRRYGQKK KKIH 204

(2) INFORMATION ON SEQ ID NO. 312:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
 (iii) HYPOTHETICAL: yes
 (vi) ORIGIN
 (A) ORGANISM: HUMAN
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

RISGCSPRSS CCFQCPADR FKKPTEQQQN EVFLRSIQKC TVPPLTRTST QVNGLSQCRR 60
 WKAAlFYVCA QPYSLLEVCLA YSNISSLSKA VHCYCQFDLH TVFPLDPCYH LDLVCVCVYV120
 CLCVCGLVWFG ETGSCTVTFG CSAVAQSRLT AALTS 155

(2) INFORMATION ON SEQ ID NO. 313:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 70 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
 (iii) HYPOTHETICAL: yes
 (vi) ORIGIN
 (A) ORGANISM: HUMAN
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AVMDQVMQFV EPSRQFVKDS IRLVKRCKTP DRKEFQKIAM ATAIGFAIMG FIGFFVKLIH60
 IPINNNIIIVGG 70

(2) INFORMATION ON SEQ ID NO. 314:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 112 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
 (iii) HYPOTHETICAL: yes
 (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

FRNRKHLERK KKNPQNIQAN LYSVFSHPH TCSPISKMKN SLPKCIQPPPT MMLLIGIWIN 60
 FTKKPBMNPII ANPIAVAMAI FWNSFLSGLV HLLTSRMESF TNCRLGSTNC IT 112

(2) INFORMATION ON SEQ ID NO. 315:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

DEKLSSKMYS ATNNNDVINRN MDQFHKEANE SHYSKSYCCC HGNLLEFFSI RFSASFNQPN 60
 GVLYKLPTWL NKLHYLIHDC LPNRHLKCQG HVALELADGG PPEPESGFLP 110

(2) INFORMATION ON SEQ ID NO. 316:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

GSSEGSYSSQ TETCPLTPSL VTGSMFAQNF LRGLSLQKSN LLPEECCLASE NLTLSFPSVN 60
 GHRCVAQGSE TSESRAQWHG VALVVRKVIG QLYCKRNKYV VQFCKCQVCS VVL 113

(2) INFORMATION ON SEQ ID NO. 317:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

KRGQLWSLN LLAPCAGYKT RSWSKIALTP NPNAVQDLGA TQPVVIVCWTF PFFVCLLVSK 60
 IALLGTAWKV QAFLLARSGL ASSPCLHSVP KEDFCSTLWS 100

(2) INFORMATION ON SEQ ID NO. 318:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

SQIISNLVDN YSIQELMFSE TVINRIFTSG LAGRLLGRKG RVEGWVAHQN GDEPGKTTML 60
 LFPLYPLKPIS RVLNDAFFVC FLIGSQISFS IKNWGYKPKE T 101

(2) INFORMATION ON SEQ ID NO. 319:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 368 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

WWRLNNKSAK VRQQAADLIS RTAVVMKTCQ EEKLMGHLGV VLYEYLGEELY PEVLGSILGA 60
 LKAIVNVIGM HKMTPPIKDI LPRLTFLKK RHEKVQENCI DLVGRIAADRG AEYVSAREWM120
 RICFELLELL KAHKKAIRRA TVNTFGYIAK AIGPHDVLAT LLNNLKVQER QNRVCCTVAAI180
 AIVAETCSPF TVLPALMNEY RVPELNQNG VLKSLSLFLE YIGEMGKDYI YAVTPLLEDAA240
 LMDRDLVHRQ TASAVVQHMS LGVYGFGCED SLNHLLNYWV PNVFETSPHV IQAVMGALEG300
 LRAIAGPCRML QYCLCQGLFH PARKVRDVYVW KIYNSTIYIGS QDALIAHYPR IYNDDKNHLI360
 IRLMNGL 368

(2) INFORMATION ON SEQ ID NO. 320:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 121 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

YPFFTLCORN RVFDISSLVYVK EMLQNVNCFK LKLPLKRPRY IYLIVYIMFN ICOSILOVCS 60
 FISIKYGYVV AQLLKWCIV YICTPNNIVC TFCFLYICCA GFFRLYQCNL CLLRYVQKMS120
 I 121

(2) INFORMATION ON SEQ ID NO. 321:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

FFFFFFFHSNVYFFFFFF FFFFFGKNNVI YLHCFHSSTV VLGLNISITL LFPIYILLEY 60
 YYKYNIQFKK TYGETQLMFF SPLYRLLSII RLQWKFIVTF SVHILKGROY TDKA 114

(2) INFORMATION ON SEQ ID NO. 322:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 597 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

EKCGQYIQQKG YSKLKIYNN LENVAEFGGL TDFSDTFKL RGKSDENEOP SVVGEFKGSF 60
 RIYPLPDDPS VPAPPRQFRE LPDSVPQEFT VRIYIVRGL E LQPQDNNGLC DPYIKITLGK120
 KVIEDRDRHYI PNTLNPNVFGR MYELSCYLPQ EKDLKISVYD YDTFTRDEKV GETIIDLENR180
 FLSRFGSHCG IPEEYCVSGV NTWADQLRPT QLLQNVARFK GFPQPLSED GSIRYVGGRD240
 YSLDEFANK ILHQHLGAPE ERLALHILR QGLVPEHVT RTLHSTFQPN ISQGKIQMWV300
 DVFPKSLSGP GPPFNITPRK AKKYVLRVII WNTKDVLDE KSIITGEEMSD IYVKGWIPGN360
 EENKQKTOHV YRSLDGEQNFN NWRFVFPFDY LPAAEQLCIVK KKEHFWSIDQ TEFRIPPRLI420
 IQIWQNDKFS LDDYLGFLEL DLRHTIIPAK SPEKCRLDMI PDLKAMNPPLK AKTASLFERQR480
 SMKGWWPACYA EKDGAARVMAG KVEMTLEIN EKEADERPAG KGRDEPNMNP KLDLPRNPET540
 SELWFTNPCK TMKFIVWRF KWIIGLFL LILLLFVAVL LYSLPNYLSM KIVKPNV 597

(2) INFORMATION ON SEQ ID NO. 323:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 76 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

IRRDKAYLTF KWRDDENPLI QSFRTKRQSS DKSMTWMKCP TGALDIFNFC DYVKEVDFTD60
 NGAEEANISKR NPNFFP

76

(2) INFORMATION ON SEQ ID NO. 324:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

FFFLYSFSSDN HDFRSFKTIY LAFVSGGELA 'NILKPAIIIV NLRTGLSWGS EGKELFEQMC60
 VGGTGFBPTA KLVLLIEISFY NTKISLCQRF 90

(2) INFORMATION ON SEQ ID NO. 325:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TRSLLYFHMF LILWEEVGIP FTNVGFCSII CKVHLFHIIA EIKDVQGPCR AFHPCHTLIR60

(2) INFORMATION ON SEQ ID NO. 326:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 42 amino acids

- (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
- (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

IRNEKKGCVL SVGEMELVLV VLEQDRHLVL MLWSFVIVEH RG

42

(2) INFORMATION ON SEQ ID NO. 327:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
- (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

ATCSDNRSKIQFLFNLECYV LLEPAICMYR INNFYSFGQV ILRQSQWIQK

50-

(2) INFORMATION ON SEQ ID NO. 328:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

PKGVVVNPGA LLSQRTTASE LSACPAPLTP GPVPSHLLIR HSLSSHSL

48

(2) INFORMATION ON SEQ ID NO. 329:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

ISEAVVNFSV LLLASVCLPI DTHYTNVPSK CSLHICFHCV PTGAMKCVRS PSSGGMSAAL 60
TTAIRIVLCG IFIYINFICT VISLFICQVT ICKSYTHKLL 100

(2) INFORMATION ON SEQ ID NO. 330:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

EAQKWDCIWT KNYKKVQLSV SRMQALALGD GSSLENAAAD SLFQRSSFER RVCYISFFT 60
TLWRLKDLVV SCFLKITGIW RFVKPFWTDI SSKYFFIKVF EGDDFLDLWL DILGFPDYIV120
LS 122

(2) INFORMATION ON SEQ ID NO. 331:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

ENWASRYFQGS SFTEQKVWVG HWLEGDSPTL TVTIWAATGG IVQLASRCIP HLKYCWIKAI 60
 YTLAKSKAKE IALDPESQQD HLIFPNQHLG QQLPSTFLFH SWFFFFFFLQ DLAVTQDGVQ120
 WHDH 124

(2) INFORMATION ON SEQ ID NO. 332:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

LNVVDLLTRR LCEKIYVVIY MICRSHFYYQ ALFSLQSHSL TVCNNSWFMLM IDKYPVFVTF60
 SNYHCNDNLS HVYTNCNFLAS FP 82

(2) INFORMATION ON SEQ ID NO. 333:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

RLVKYKNSLN REKASQVFPL KVKYGTFHEN KVNDFKNLTF FRRKKKTSYE PSLVNHLVYK60
IFPLFKKCFC KILRSHEIMP WS 82

(2) INFORMATION ON SEQ ID NO. 334:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 75 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

KLEYIMSTAN CSFCLILTDY AFPQRSSRSH IYRHIYGSGL KEKTILSSIM IYHCAINQKN60
QVRNTIKTTL KGKNF 75

(2) INFORMATION ON SEQ ID NO. 335:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 72 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

NEYCSWSTCI KQKTCQLLGA NTQNLVPVFF FFLTTIVYTF LKIKFVTKSP MSFTCIYDHQ60
MVIRATYVNA CL 72

(2) INFORMATION ON SEQ ID NO. 336:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 93 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

THNTSTITAY RKLQSTLQAS KVHSVAQSPW RGRDLKVLM S SYFTCFLLST QCKMNFLHSL60
 YFRLKIDSFL VLTLTLEGTV VPGKRSRFTV PNH 93

(2) INFORMATION ON SEQ ID NO. 337:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 99 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

LGPRGEIEVY LAKSLAEKLY LCQYFVRPAS MTYDDIPHLS AKIKPKQQKV ELEMAIDTLN60
 PNYCRSKGEQ IALNVDGACA DETSTYSSKL MDKQTCFSS 99

(2) INFORMATION ON SEQ ID NO. 338:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 56 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GKSRRSACPS ASRNTCWSRR RRRPRRSQAS APLCCGNSWG SGCRWPSQAL PSAAWA 56

(2) INFORMATION ON SEQ ID NO. 339:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 59 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

GRAEGLLVHQ LRGIRAGLVG AGPVHVQRNL LPFAAAIVGV QGVGDGHLY LLLLGLDLG 59

(2) INFORMATION ON SEQ ID NO. 340:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 157 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

QPSSLLHHCP YPYPPRHLLA TPPLLKPQLLA GSPAHASLIS FLASPQRASR QHGGPSQRAG 60
 TLSCLPVELG GSSEGRGLCH GSADPTNRAA EPQERGEPAAG DRRPLPEWG RVSLAESPGA120
 EFRCPGSLGE WGEIPEKESS AHPKTEEEAL CPAPGSH 157

(2) INFORMATION ON SEQ ID NO. 341:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 260 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

NHSCWQGPQL MPASSPFLLA PKGPPGNMGG PVREPALSVA LWLSWGAAALG AVACAMALLT 60
 QQTTELQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS RKRRAVLTQKL20
 QKQQHSVLHL VPINATSKDD SDTVEVMWQP ALRRGRGLQA QGYGVRIQDA GVYLLYSQVL180
 FQDVTFTMGQ VVSREGGQRQ ETLFRCIRSM PSHFDRAYNS CYSAGVFHLH QGDILSVIIP240
 RARAKLNLSL HGTFLGFVKL 260

(2) INFORMATION ON SEQ ID NO. 342:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 201 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

TPASWIRTPY PWACRPLPLR RAGCHITSTVT SESSLEVALM GTRCRTECCF FCFWVSTALL 60
 FRDLSPLSQA SRASELCSGR LCQGYPSFW EGPPVPCSRL TSLLRLCSSV CWVSRAMAQA120
 TAPRAAPQLN QRATESAGSL TGPPMLPGGP LGASKKGDEA GMSWGPCQQL WFQEWSKEV180
 AGRVRVRAVV QKGRRLLRK E K 20*

(2) INFORMATION ON SEQ ID NO. 343:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 165 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
 (iii) HYPOTHETICAL: yes
 (vi) ORIGIN
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GRRSRMIEIPV PVQPSWLRRA SAPLPGLSAP GRLFDQRFGE GLLEAELAAL CPTTLAPYYL 60
 RAPSVALPVA QVPTDPGKFS VLLDVKHFS EETAVKVVGZ HVEVHARHEE RPDEHGFVAR120
 EFHRRYRLPP GVDPAVTSA LSPEGVLSTIQ AAPASAQAPP PAAAK 165

(2) INFORMATION ON SEQ ID NO. 344:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 116 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
 (iii) HYPOTHETICAL: yes
 (vi) ORIGIN
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TALAQPQASQ AQSPHPPNVL DCTDLPLQTI QAWFPRPDS PATRQSTTAP SSPPFSAVKEQ 60
 PATPDGSTLF RLPQLLDTRP TRTPNTKLRY LSHPNLPRLC TDVLGPLPNS NQTPSP 116

(2) INFORMATION ON SEQ ID NO. 345:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 111 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
 (iii) HYPOTHETICAL: yes
 (vi) ORIGIN
 (A) ORGANISM: HUMAN

TRANSLATED BY EMBL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

DIRAESGEVG VGESVQFGVG CSSWPGVQEL GQSKKGSRVW CGWLGFHGRK WAGGGSCRLS 60
 GCRGRIGSWE PGLDGLENEV CAVQDVWGVG GLCLTGLGLG QGCLHHNLVS K 111

(2) INFORMATION ON SEQ ID NO. 346:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

RTEEEKKKKE KNQQPQLPTP KCWSFYVKGR IPGYGHGVYK YVGRFSANSE PTV 53

(2) INFORMATION ON SEQ ID NO. 347:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

NELKWTNRAE LSVGWQSWKF AFPASHQLNE VSMSIQLRLF FKNNHAFLNP N 51

(2) INFORMATION ON SEQ ID NO. 348:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

RHAGGGALGN LPPQPGSGV MHPETCPSTL LASPLPHSIA PGLFLLDFVL VLALFLIFFY 60
 YESPGRGDS GSWPGPGRQV ALEMGKCLCR GAELSLCFSF FPLLLPLHTP VAGRNLGFPE120
 SLGVPPFLPH PGGTPRAPGL FLLLFSIEWAV 150

(2) INFORMATION ON SEQ ID NO. 349:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

RSFLTRSVIK LPKRKTRGET SPGPWAFLPG GVRRVGPPSF QGSRGSFQPR GCEGEGVEEK 60
 RNRERAQRRL DDTFPSPGP PAVLAQASSH CHLCVQEIHNN KKKSKTCKPK KQNPKGKD LG120
 QWNEEEGRRG R 131

(2) INFORMATION ON SEQ ID NO. 350:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

RKKGETEREL SASTQTLSHL QGHLPSWPRP APTVTSASRR FIIKKNQKQS QNQNQKIQKEK 60
 TWGNNGMRKG GEEGRAGLW MHNSRARGLG RKIPQRPAAC VALARHVVFG GRLPIHPVEI120
 LVAGLLGGVK PVSDRQAGKG LGDGGCGRER V 151

(2) INFORMATION ON SEQ ID NO. 351:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

TLTAAHEGRGG KCTEEGDASQ QEGCTLGSDP ICLSESQVSE QEEMGGQSS AAQATASVNA 60
 EEKVARIHE CQWVVEDAPN PDVLLSHKDD VKEGEQQGQES FPELPSEE 108

(2) INFORMATION ON SEQ ID NO. 352:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

KFFGNSLHAT PKCTPITLWL FSEKDFSQIV PFTPLRAALG NSPDHLLPPS RHLCVTAGHP60
 GLEHPPPPTD THEYGLP 77

(2) INFORMATION ON SEQ ID NO. 353:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 122 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

TYSIHLHSQT KLKSLKVHKK IAQLKSAEYT QNCHPTVFSV FPAAILFPPQQT SSAPSHPKYA 60
 IVFVILIKIL KQKFIVEQFM STRVKCLSCSC PVCISSGFII QIKKILKNFL VTACMQPLSV120
 PL 122

(2) INFORMATION ON SEQ ID NO. 354:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 457 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

PVCEPLSCGS PPSVANAVAT GEAHTYESEV KLRCLEGYTM DTDTDFTFCQ KDGRWFPPERI 60
 SCSPKKCPLP ENITHILVHG DDFSVNRQVS VSACAEYTFE GVNVISVCQLD GTWEPPFSDE120
 SCSPVSCGKP ESEPEHGFVVG SKYTFESTII YQCERGYELE GNRERVCQEN RQWSSGGVAIC180
 KETRCETPLE FLNGKADIEEN RTTGPNVVYS CNRGYSLEGP SEAHCTENGTE WSHPVPLCKP240
 NPCPVFFVIP ENALLSEKEF YVDQNVSIKC REGFILLQGHG IITCNPDETW TQTSAKCEKI300
 SCGPPAHVEN AIARGVHYQY GDMITYSCYS GYMLEGFLRS VCLENGTWTS PPICRAVCRF360
 PCQNNGICQR PNACSCPEGW MGRLCEEPIC ILPCLNGGRC VAPYQCDCPP GWTGSRCHTA420
 VCQSPCLNNG KCVRPNRCHC LSSWTGHNCS RKRRRTGF 457

(2) INFORMATION ON SEQ ID NO. 355:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 210 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
 (iii) HYPOTHETICAL: yes
 (vi) ORIGIN
 (A) ORGANISM: HUMAN
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

GVRAASKEIE ELRRRAHREGT SRAVTGEGPA AGRMTVPKQT QTPDLLPEAL EAQVLPRFQP 60
 RVLQVQAVQV SQTQPPIPST DTQVQPKLQV QAQTQTSFEH LVLQQKVQVQ PQLQQEAEFPQK120
 QVQPVQVQPA HSQGPQRQVQL QQEAEPLKVQ QPQVQPQAHF TAPRAGAAAA EEAGPDTDFSI80
 TGAHTGHHSQA SRHRELLPGV VFSFRPPGAG 210

(2) INFORMATION ON SEQ ID NO. 356:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 292 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
 (iii) HYPOTHETICAL: yes
 (vi) ORIGIN
 (A) ORGANISM: HUMAN
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GRAGRATATMF SQQQQQQLQQ QQQLQQLQQ QQLQQQQQLQQ QQLLVLQQQLL QQSPPPQARCH 60
 GVGGGPPQQP QQPPLNLQGQ NSASLLNGSM QRALLLQLL QGLDGFAMPP ATYDTAGLTM120
 PTATLGNLRG YGMASPGLAA PSLTPPQLAT PNLLQQFPQA TRQSLLGPPP VGVPMNPSQF180
 NLSGRNPQKQ ARTSSSTTPN RKDSSSQTPM VEDKSDPPEG SEEAAEPRMND TPEDQDLPFC240
 PEDIAKEKRT PAPEPEPCEA SELPAKRLRS SEEPTKEKPP GQLQVKAQPP AG 292

(2) INFORMATION ON SEQ ID NO. 357:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 169 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

PRLPSVAVG MVRPAVSYVA GGIANWSSPC NCCKSKALCR MEPLRREAEI VPWRFRSGCC 60
 GCCGGPPLTP WQRACGGDCW SSCWCSNCC CCNCCCWSCC CCNCWSCCCC CWSCCCCWL120
 NMVARLPARP QRSSRPHGWA GPAAPTFRPG GSGPRAPGLP AATPGPVGS 169

(2) INFORMATION ON SEQ ID NO. 358:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 158 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

ISKTKKYCGS PSSRIRLEGG HLEMRKARGG DHVPVSHEQP RGGEDAAAQE PRQRPEPELG 60
 LKRAVPGGQR PDNAKPNRDL KLQAGSDLRR RRRDLGPRAE GQLAPRDGVI IGLNPLPDVQ120
 VNDLRGALDA QLRQAAGGAL QVVHSRQLRQ APGPPEES 158

(2) INFORMATION ON SEQ ID NO. 359:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 119 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

QSLRTLNKKN KKVLWISLEP NSARGRSPGD EKGPRGGPCA CVPRAAERRG GRCCPGQAQE 60.
 ARARAGAQTS CPGGPEAGQC QAQPGPETAG WLRPPEATAG PWPSCRGSAG PEGWGHWP 119

(2) INFORMATION ON SEQ ID NO. 360:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 187 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

PPEFGWDAAE TDLLLAEEGS GWRGPHGQQV LGLLWRPRLR SKLPAVDHLO SSPRSLAEGLG 60
 IQGATEEVHHL DIRQGVKAND DPIPQRGQLTL CMRAKVPPSP PEVGASLQFQ VPVGLGIVRP120
 LAPRDSSFEP QLWLWPLPGL LGSSVLPASR LLVGHRRHMVP PAGLSHLQVT ALEPNSARGR180
 STVLFCF 187

(2) INFORMATION ON SEQ ID NO. 361:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

STIILGKSRI EFFSRCPTRV QQGPQSRLIN SHRIQTGKTI ALRSQQLLSSL YGSRKNSTKM60
 TGHPMMSVMPM KPHLLEKPLN QNYLF 86

(2) INFORMATION ON SEQ ID NO. 362:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

SEARCHED = UNSEARCHED

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

ITKAIVFSEV FSSGYTVEVR ESLILLLGAI IKAMQQPKIK HFGSSQDDMS GDRSCGSHSN60
 NLMGPEEKTG VNVLSSFYMQ ELC
 83

(2) INFORMATION ON SEQ ID NO. 363:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

YKNDRSSYER HANETPSSGE ALESELSFFL MSSDAASFLI FLKTVFCGGM YICTPNYLAL 60
 GNHSTTQRQL NKEKFNFKYQ VLSNISQTSD FIKGLPANKV HPKYTGKAR LLQGPRV 117

(2) INFORMATION ON SEQ ID NO. 364:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

SCRCFYCMRD MPLTREWRTLP NSPRMTRRHS HVICIFSYQL QIVALLRLPP VQQEMERKHF60
 SFLHTTPLDN WKYFWWVITIL GYF
 83

(2) INFORMATION ON SEQ ID NO. 365:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 144 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

QYGPSRVEE MSYRIANTLG SFLPRLAQSR QQQQNVEDAM KEMQKPLARY IDDEDLDRML 60
 REQEREGDM ANFIKKNNAK ENKNKKVVRP YSGPAPPNR FNIWPGYRWD GVDRSNGFEQ120
 KRFARLASKK AVEELAYKWS VEDM

144

(2) INFORMATION ON SEQ ID NO. 366:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 116 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

KPTKHRCCQH PKKYRYLNPN IRSRIFFCGQ NWHSTSCWSV WAPIISTDNC YHWISRCLCP 60
 LPQPSHPHSI RKVTYPQHSI CRQVPPLPSC WQAWQSASVQ IHWICPLRPS DIQARY 116

(2) INFORMATION ON SEQ ID NO. 367:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 160 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

SSENPPNTAA VNTPRSTGTS IQTSGLEYSS VVKTGIQQVA GLCGLQLLAQ TTVTGYLAA 60
 YAHYHSPATP TASGKLHLN TPFVGKFLHC LLAGKPGKAL LFKSIGSVHS VPAISRPDIK120
 SVGRRCWTTV ARSHFFILVL LGILLDEVG HRVPLSFLS 160

(2) INFORMATION ON SEQ ID NO. 368:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 227 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

WESMNRWYVK PLETSSSKVK AKTIVMIPDS QKLLRCELES LKSSQLQAQTK AFEFLNHHSV 60
 MLEKESCLQQ IKIQQLEEVL SPTGRQGEKE EHKGWMEGQR QELYGALTQG LQGLEKTLRD120
 SEEMQRARTT RCLQLLAEI RDSKKFLWEE LELVREEVTF IYQKLQAQED EISENLVNIQ180
 KMQKTQVKCR KILTQMKQQG HETAACPETE EIPQEPVAAAG RMTSRRN 227

(2) INFORMATION ON SEQ ID NO. 369:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 155 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

TRANSLATED BY ROBERT D. BROWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

FIFSLLEGSSG RAVPAAQAGG KGGALLKGG WERSWSESES ESEQEGSGGLR HWCPPLWPLRL 60
 EALGQAPEHK VRLSMEFCST CTADHISLSS FWRSRFQQPL APAVSLQSPD RRLSHDFAAS120
 SWSGFCGISP AFSAFSECSP SSLRSHPPAL GASDR 155

(2) INFORMATION ON SEQ ID NO. 370:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

DLILLRLELL IDEGHLLPHQ FQLLPQELLA VPDLLGQQQLQ AASGAGPLHL LTVTQGLLQP 60
 LKALGQQPIQ LLPALLHAPL VLLLLSLAAC GAQHLFKLLN LDLLQAALLL QHGH 114

(2) INFORMATION ON SEQ ID NO. 371:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 201 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

TASTLRAVFP RPASESPPLR ARSDAEDLTA AMSSNECFKC GRSGHWAREC PTGGGRGRGM 60
 RSRGRGFQFV SSSLPDICYR CGESGHLAKD CDLQEDACYN CGRGHHIAKD CKEPKREREQ120
 CCYNCGKPGH LARDCDHADE QKCYSCGEFG HIQKDCTKVK CYRCGETGHV AINCSKTSEV180
 NCYRCGESGH LARECTIEAT A 201

(2) INFORMATION ON SEQ ID NO. 372:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 189 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

LATAATVVDFT CLAAVGDMT SFTTPIALHF GAVFLNVSEF STRIAFLLLIC MVAVTSQMAW 60
 FATVVAALLS LSLGLLAVLG NVATSTAVIA GILLKITILG KMTRLTTAIT NIWKRRGNKL120
 ETSATASHST TTASTSRTEP GPVARSSGLE ALIAAHGCSQ IFRVGAGPQR RRLGRRPGED180
 GSQGRGCLEF 189

(2) INFORMATION ON SEQ ID NO. 373:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 316 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GGDPVVSSSY RSGCSEQKQ PASSDVVLPA TMSYTGFVQG SETTLQSTYS DTSAQPTCDY 60
 GYGTWNNSGTN RGYEGYGYGY GYGQDNTNY GYGMATSHSW EMPSSDTNAN TSASGSASAD120
 SVLSRINQRL DMVPHLETDM MQGGVYGSGG ERYDSYESCD SRAVLSEERDL YRGDYDYESL180
 DPEMEMAYEG QYDAYRDQFR MRGNNTDFGPR AQGWARDARS GRPMAAGYGR MWEDPMGARG240
 QCMSGASRLA LPLLBEEHHPR VRHVPGACEV GAPSGRAASRF GFRVWQWHEA DEGGLGRRGP300
 QPICEPRRRR ESRAAF 316

(2) INFORMATION ON SEQ ID NO. 374:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 200 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

I PAA LLTGSI RMP PCFLFFF LVR KSA VVPV FPVR PHLLHA IAKP ENQ NGK PPGKA PQPRM 60
 PLE HAVL GDD VLGE EGG QAE RH QTCT GP GP PWGL PTCAHS LRPL AGRSGH PGPS PVPW DR120
 RCR CHAC GTG RGR HRIG PHR PFPS QQQ ARC SHSL TGTR A HS GRPSS RRT HKS HTFL HLS180
 RT RL LASCLS PNA APYLSAG 200

(2) INFORMATION ON SEQ ID NO. 375:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 218 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

STSH DCVPQA DAAAYS R TAD GETEAR GGRG GADLPAS PSP RPR LAPP WPV RSTR GARR RR 60
 TAR GQAG SSS AMAA QRLG KRV LSKL QSPSR ARGP GGSP GPG LQKR HARV TV KYDR RELQ RR120
 LOVE KWI DGR LEELY RGMEA DMPDE INIDE LLELE SEEER SRKI QGLL KS CGKP VEDFI Q180
 ELLA K LQGL H RQP GLR QSP SP SHDG SLSFLQ DRARTA RP 218

(2) INFORMATION ON SEQ ID NO. 376:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 112 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

NQLKLKQQAG SFSQEGCKGE NILSFLLQGN HCPGVPASGR HNLSKVQGML ARKGGILDCC 60
 LLSESPPTPQ PASWCLFSSK LSLPNLSSSE GKRESVPGES RVGERTGKGT DI 112

(2) INFORMATION ON SEQ ID NO. 377:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 96 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

VRPEHSLMVL SLDTPTSYLQ FSRRRASGTL GCKPNLGSMF ALNPNSQRSS ECIFHHAAAG60
 CWPRFCVFSQ PSEITSFLVA VTNSSWTMKG LIYFP 96

(2) INFORMATION ON SEQ ID NO. 378:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 145 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

SNRLVASP KK DARVKTFFPS FCREIIALVC QPVVGTTFQK FKGCWLEKEV FWIAASSQNP 60
 LLPHSLPPGV FFPNNSLYLT SLHQKASGNL FRVSVEWEKG QAKAQIFRRE SSYFWPLHVP120
 YSGIVGPDDW HSOSQLWFWE NIRGS 145

(2) INFORMATION ON SEQ ID NO. 379:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 429 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

RQFEITSISV DVWHILEFDY SRLPKQSIGQ FHEGDAYVVK WKFMVSTAVG SRQKGERSVR 60
 AAGKEKCVYF FWQGRHSTVS EKGTSALMTV ELDEERGAQV QVLQGKEPPC FLQCFQGGMV120
 VHSGRREEEE ENVQSESWRLY CVRGEVPVEG NLLEVACHCS SLRSRTSVMV LNVNKAFLYL180
 WHGCKAQAH KEVGRTAANK IKEQQCPLEAG LHSSSKVTIH ECDEGSEPLG FWDALGRRRD240
 KAYDCMLQDP GSFnFNAPRLF ILSSSSGGDTA ATEFVYPPARA PSVVSSMPFL QEDLYSAPQP300
 ALFLVDNHHE VYLWQGWWPI ENKIGSARI RWASDRKSAM ETVLQYCCKGK NLKKPAPKSY360
 LIHAGLEPLT FTNMFPWSWEH REDIAEITM DTEVSNQITL VEDVLAKLCK TIYPLADLLA420
 RPLPEGSIL 429

(2) INFORMATION ON SEQ ID NO. 380:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 169 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

TRANSLATED FROM ENGLISH

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

DVFHEGDLIG NFRVHLCDLS DVLSVLPGAK HIGECQGLQT SVDKVRLGGW FLEIFSFAVL 60
 EHSLHRTLPV GGPADAGGT DLVLDGPPAL PEVHLVVIVN KEKCWLGRAV QIFLQEKGHT120
 DHRGGSGRVH KLCGCKIPRG AAEDEQAGRE VKTSRILKHA IVGFFVSPS 169

(2) INFORMATION ON SEQ ID NO. 381:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 234 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GIPSEWLG A FITLVYCDFA ATMQSCFQGT LFLDLVRSGP SDLLRVGLGF ASVPQVDEGL 60
 VDVKHHGSS GPQAATVTGH FQQIFFHGHL STHAVQPPLT LHIFFFLFPP PRVHHHPPL120
 TLQETGGLLS LENLDLGPPF LVQLHRHQRR RALLTHGGVP ALPEEVDA LL FAGCPHRVLS180
 LLATSHCRAH HELPLDHIGI PLMELPDALF GEPAIVEFQD VPDIHGNAGD LKLP 234

(2) INFORMATION ON SEQ ID NO. 382:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 81 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

RLFAPLRTSW AVVIPGARVA LCFYKIMTYV TCLHVCLLVE FLNSQLTNHR KYYFLSYGFW60
 FTGLRGFSEY LWPQQHTQFP S 81

(2) INFORMATION ON SEQ ID NO. 383:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 61 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

IVNRRTACTL FEVNLEWKAR DYTLLFKIDIC GAHTIYEIVP SKKEKKKIRR SNLEQHCLIK60
 A 61

TRANSLATED FROM PDB

(2) INFORMATION ON SEQ ID NO. 384:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 56 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

PPDFFFLFFR GYYFIYCVSP TNVYFKKSIV PGLPFQIHLK ESTCSSPVYN LIEMRK 56

(2) INFORMATION ON SEQ ID NO. 385:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 139 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

LDSSHCCSCS TALFRQTAA AAVPRMVIRV YIASSSGSTA IKKKQQDVLG FLEANKEIGFE 60
 EKDIAANEEN RKWNRRENVP ENSRPATGYPL PQQIFNESQY RGDYDAFFEA RENNAVYAFL120
 GLTAPPSKE AEVQAKQQA 139

(2) INFORMATION ON SEQ ID NO. 386:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

ETKHILLFL NRCRARCRCN IYTDHHFGNS GCGCLGPEKG CGAAAAMAGI QLGAETAVGR60
 EGWGKVEGEL ARAPPPLA A STELSKRCS SPKPR 95

(2) INFORMATION ON SEQ ID NO. 387:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

FCIHFECLHV KTQLIYYFNI KPISEFAKLI LLFYKSNGDS FFRMLKAQCL RFMLAALLAL60
 LLPLNQVGLS SLRRHTLHYF LWLQRRHHSP RDTGFH 96

(2) INFORMATION ON SEQ ID NO. 388:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 221 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

FIMLNIIK FSSFSIRCAI LSSVCLNEAI TFAFLLQVFL WNMDKYTMIR KLEGHHHDVV 60
 ACDFSPDGAL LATASYDTRV YIWDPHNGDI LMEEFGHLFP PTPIFAGGAN DRWVRSVSFSI20
 HDGLRVASLA DDKMVREWRI DEDYPVQVAP LSNGLCCAFS TDGSVLAACT HDGSVYFWAT186
 PRQVPSLQHL CRMSIRRVPMP TQEVCQELPIP SKLLEFLSYR I 221

(2) INFORMATION ON SEQ ID NO. 389:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 118 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

KGGATCPESP QDRKRRGNLD MEKLYSENEG MASNQGKMEM EEQPQDERKP EVTCTLDDKK 60
 LENEGKTENK GKTGDEEMLK DKGKPESEGE AKEGKSEREG ESEMEEVERE GTRGRGSG 118

(2) INFORMATION ON SEQ ID NO. 390:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 138 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

RFPYLGFFPLS RPPPSLTLP SLTFLLLPLP HSLAFLYPLT FPHLLFCPCF LSFPFRFLTSC 60
LPEYKLLAFA SRLVAVLHFP SFGLGKPFHL FHCRVPCRD FFSFSCPAGI LDRLLLLFSF120
AERWEQQTRR PGRSWTKN 138

(2) INFORMATION ON SEQ ID NO. 391:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3218 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

TRANSLATED BY COMPUTER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

(2) INFORMATION ON SEQ ID NO. 392:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

GTGAGGGACA GATGGACAGA ATGCAGAGGT ACATAGATGA GCTGAGGCTG ATCCAGCTCC 60
 CCTGAAATTG AGAGTGTAA CTTTGAGAC CCTGACAAAT CTCTTGGTGC TATCTAGCCA120
 TTGCCCCCAT TTTTTTTTAA AAGGCCATCT GAATTCCTA TTGTATGGT GGGAAAGCAATT180
 TTGGATATGA TGCAAGGAAT CTCTTCCCTGG AGTCAAAAGT TCCCAAGAGG TCCTGTATTT240
 TTAAGAAATG GAATTTATT AAATAATATT TAAGCTTGTG CCCATGTTGG CGGGGCAACT300
 TTTTCAATG GTGCTTATTA GAAGAAGTT TTTCATCTTG TCATTTTAAG AAAATAAAAAC360
 TGGAAATTGA ATATGGGTGG CATGATTGTA CCCTTTTACTG TCTCTTATTI TTCTACTCC420
 CTGTCCTCT ATAATCTATGC CATACTATTA GATGCTGGTC CACTGAATGC TGAGATGATC480
 TTGGTTTTGG GGTTTTTTTTT TTAAAGAAA TATTTCACTG GTTTTTCTGT GACTCTCTAA540
 ACACCTCATG GAAACTAGGA AGACTGATT ATGAGGGAAA CTATTTGGGA TTAGTGCCAA600
 GAAACGATGA AATCTTATAG ATCTTTGAC AGTTTCTCTG TTAGGGGGA GCCTAGGACT660
 GATATCCAAG TTCTCTCCAT ATCCAAGCTT CATTGGGGGA CCCCCATTTG GCTTTAACAG720
 750
 GTGACCCGGC CCTCTTTACC GGCGCTTCCAG

(2) INFORMATION ON SEQ ID NO. 393:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

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CACGAGGAGC CCGGGAGCTGG AACCCCTCTT TTGAGAGAAGG TTGCCTGACT CAGAGACACA 60
GAAACGGTC CAGGGATGGG GAGAGATGTG GAGTGAGGGGA AGGTTTGCAAT TTGAGAAAGG120
AAGTTCGAGA ACACACTGGG ACATTGTAAC ACATTTGAAC CATCTCTGATAGAAAGGTG180
TTGGCTCTCTT AATAATGGGA GGTCAGGGCC AGGTCTCGG GCATAGGGGAG AGGGTCCGGA240
GAATGCTGCA GACCCCTGCC CACTGCCAAC GGTCTCCCTT CCGTGCACCT GCCTCTGATG300
GTGCAGGCTCT GATTCCTGTT CTCTCTCAT TGCAAGATTAA TGAAGGTGCC TACCATGTTCT360
TCCACAAGGA GCTTCTGAA GTCAACCAACT CGGTCTTCCA TGAAATAAAC ATGTGGGTCT420
CTCAAAGGAC AGCCACCGCA GGAACCTGGT CCCCACCTG AATGCATTGG CCGGTCCCCG480
GCTCATGTC TGGGGATGC AGGCAGGGGA AGGGCAGAGA TGGCTTCTCA GATATGGCTT540
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GCAAAA

546

(2) INFORMATION ON SEQ ID NO. 394:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2453 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

CCTGACGGGA CCAAGGGCGG GGGAGTCTGC GGTCGTTCCC TCGGCTGTGG ACCGGGCGGC 60
 ACGACGGCGT GCAGGGTAAC ATGGCGGTG CGGAAAGTAT TATTTCGCA AAGAAACATA 120
 AGAAGAAAAA GGAGCGGAAG TCATTGCGAG AAGAAGATGT AGCCGAAATA CAACACGCTG 180
 AAGAATTTTT TATCAAACCT GAATCCAAG TTGCTTAAGTT GGACACGCTC CAGTGGCCC 240
 TTTGCTAAA GAATTTGAT AAGCTGAATG TAAGGACAAC ACACATACCA CCTCTTGCAAT 300
 GTGGTCAAA TCCTCTGAAG AGAGAGATTG GGGACTATAT CAGGACAGGT TTCATTAATC 360
 TTGACRAAGCC CTCTAACCCCC TTCTTCCCATG AGGTGGTAGC CTGGATTCTGA CGGATACCTC 420
 GGGTGGAGAA GACAGGGCAC AGTGGTACTC TGGAATCCCAA GTGACTGGT TGTTTAATCG 480
 TGTGCATAGA ACGGCCACT CGCTTGGTGA AGTCACAAACA GAGTGCAGGC AAAGAGTATG 540
 TGGGATTGT CGGCGTGCAC AATGCTATTG AAGGGGGGAC CCAGCTTTCT AGGGGCCCAG 600
 AAACCTGAC AGGTGCTTCA TTCCAGCGAC CCCCACTAT TGTGCTGAGTA AAGAGGCAGC 660
 TCCGAGTGAAG GACCATCTAC GAGAGCAAAA TGATTTGATAA CGATCTCGAA AAGAAGATTAG 720
 GAATCTTTTG TGFTGAGTTG GAGCTGCGA CCTACATTGAC GACATTATGT GTGCAGCTG 780
 ATCAGTCAG CGCAGGAGT ACGTGCTAGT CAGGAGCTTC GGAGGGTTCG TTCTGGAGTC 840
 ATGAGTGAAGA AGGACCAACAT GGTGACAATG CATGATGCTGC TTGATGCTCA TGCGCTGTAT 900
 GATAACCARCA AGGATGAGAG TTACCTGGCG CGATTTGTTG ACCCTTGGAA AAAGCTGTG 960
 ACATCTCATCA AACGGCTGGT TATGAAAGAC AGTCAGTAA ATGCCATCTG CTATGGGGCC1020
 AAGATTATGC TTCCAGGTGT TCTTCGATAT GAGGACGGCA TTGAGGTCAA TCAGGAGATT1080
 GTGGTTATCA CCACAAAGG AGAACGCAATC TGCGATGCTA TTGCAATTAT GACCACAGGG1140
 GTCATCTCA CCTGCGACCA TGGTATAGTA GCCAAGATCA AGAGAGTGTAT CATGGAGAGA1200
 GACACTTACCG TCTGGAGACTG GGGTTTAGGT CAAAGGGCAA GTCAAGAGAA GCTGATGATC1260
 AAGCGGGCC TTCTGGACAA GCATGGGAG CCCACACAGCA GCACACCTGC CACCTGGAGA1320
 CAGGAGTATG TTGACTACAG TGAGTCTGCC AAAAAGAGG TGTTGCTGA AGTGTAAAAA1380
 GCCCGCGAGG TAGTGTGCGA AGCAGCAAA ACTGCGAAGG GAAGCGAGGA GAGTGGAGT1440
 GAAAGTGCAG AGACTCTCTC AGCGACTCTC CAGTTGATCA AAGAAGAAA GAAGAAGAGT1500
 AAGAAGGACA AGAACGGCAA AGCTGTGCTG GAGAGCGGGG CGAGGCTGG AGATGGGGAC1560
 ATGTATACCA CAAAGAGAA GAAGAAGAAG AAGAAGAGAA AAGAGGTAGA ATTGGTTCT1620
 GAGTAGTGAAG GGCCACTTGA AGCTGGAGG GAAACATTAAG CCTTATTGAG AAAACATGTT1680
 ATAGATCCTT TTGTTGCTGA GAGAGTGAA CATAGGTCCT AGACAGGGTG AAGAGTTCTG1740
 GCACATTTTA GCTGCTACTT TSAGACCTCG GTGATGTTAC CTGGTGTGGT CATCCCATCT1800
 TGTCTGTGTT TAAGGATATG GGTGGTGAAG GATGAARGAG CGACAGTTA TCCCAATGAC1860
 TTCTCTGTGTT GAGTTGGAA GCCTCACCT CAGACCGAGT AACTGTCGG AGCTGTCGC1920
 TAGTGGTTGT CTTAACATCG TAGTCTCTAGT TTGCAATTTC TAAATCCCT CTGTTAAAAA1980
 GGTTGTTAAA CAAACACAA AAAACTAAGT CTGCTCATG AAATGCTGTA GAACCTAAAC2040
 TAAGTGGTAG AAGAGTGTCA CTGAATTTC TCTCTGAAATT CAGTATAACT GAGTTTGTG2100
 CATGCTGGT TCTGGTTAT AGGCGTGTAG GGCGCTGGTAG TTTCCTACCT TGTTCTGGCC2160
 TAGAGGTCAG TCTCTTGCAC TTCCCTAAAGT CTTGTGATCA GTGCTACCT AAATCCATCT2220
 GACTACTGT TCTCTGTGCC TTCTGTTTA GGCGCTGGTTT ACTTTAAAAA AATGAAATG2280
 TTCATTGCTG GGAGAAAAT GTTGAATT TTACTTATTA AAGTCACATT GTTAAGTTT2340
 TTATGTATTC CTGTTGGGT TTCTTGTGA TCTCATGCTA GCAGAGCAA AATTGAAAAA2400
 TATTTGATT AAAATCTAG GGACCTTAT GTCCTATTG AAAAAAAAAA AAA 2453

(2) INFORMATION ON SEQ ID NO. 395:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2706 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

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GGGAGGAAGG AGACTACACC TGCTTGTGCT AAAATCAGGT CGGGAAGGAC GAGATGAGAG 60
TCAGACTCAA GGTGGTGACA GGGCCGCCA CCATCGGAA CAAGACTTAC TTGGGGTTTC 120
AGGTGCCCTA TGGAGACGTG GTCACTGTAG CCTGTGAGGC CAAAGGAGAA CCCATGCCA 180
AGGTGACTTG GTTGTCCCCA ACCAACAAAGC TGATCCCCA CTCTCTGAG AAGTATCAGA 240
TATACCAAGA TGGCACTCTC CTTATTCTAGA AAGGCCACGG TTCTGACAGC GGCAACTACA 300
CTCTGGGT CAGGACACGC GGGGGAGAG ATAGGAAGAC GGTGTGGATT CACGTCAACG 360
TCCAGCCACC CAAGATCACR GGTAAACCCC ACCCCATCAC CACCGTGGG GAGATAGCAG 420
CGGGGGCGAG TCGGAAGCTT ATTTGAGTCA AAGCTGTGAAAG CATCCCCAAC CGGAGGGTGT 480
TATGGGCTTT TCCCGAGGGT GTGGTTCTGC CAGCTCCATA CTATGGAAAC CGGATCCTG 540
TCCATGGCA CGGTTCCCTG GACATCAGGA GTTGAGGAA GAGGGACTCC GTCCAGCTGG 600
TATGCATGGC ACGCAACAGG GGAGGGAGG CCAGGTTGAT CCTGCAGCTC ACTGTCTCTGG 660
AGCCCATGGA GAAACCCATC TTCCACGACG CGATCAGGGA GAAGATCACG GCCATGGGG 720
GCCACACAACA TTCAAGCTCA ACTGCTCTGC CGCGGGGACCC CGCACACCCA GCCTGGTGTG 780
GGTCTTCCC AATGGCACCG ATCTGCAGAG TGGACAGCAG CTGCAGCGCT TCTACCAAA 840
GGCTGACGGC ATGCTACACA TTAGGGTGT CTCCCTCGGTG GACGCTGGGG CCTACCGCTG 900
CGTGGCCCGC AATGCGCGCTG GCCACACGGG GAGGCTGTC TCCCTGAAGG TGGGACTGAA 960
GCCAGAAGCA AACAAAGCAGT ATCATAACCT GGTCAAGCATC ATCATGCTG AGACCCCTGAA1020
GCTCCCTGC ACCCCCTCCCG GGGCTGGCA GGGACGTTTC TCCCTGGACGC TCCCCAATGG1080
CATGCATCTG GAGGGCCCCC AAACCTGGG ACGGGTTCTC CTCTGGACCA ATGGCACCT1140
CACGGTTCTG GAGGGCTCCGG TGTGGACAG GGGTACCTAT GTATGCAGGA TGGAGACGGAA1200
GTACGGCCCT TCGGTCACCA GCATCCCCGT GATTGTGATC GCCTATCCTC CCCGGATCAC1260
CAGCGAGGCC ACCCCGGCTCA TCTACACCCG GCCCCGGGAC ACCTGAAAC TGAACTGCA1320
GGCTATGGGG ATTCCCCAAAG CTGACATCAC GTGGGAGTTA CGGGATAAGT CGCATCTGAA1380
GCCAGGGGTT CAGGCTCGTC TGTATGGAAA CAGATTCTT CACCCCCAGG GATCACTGAC1440

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CATCCAGGAT GCCACACAGA GAGATGCCGG CTTCTACAAG TGCATGGCAA AAAACATTCT1500
 CGGCGTGTAC TCCAAAACAA CTTACATCCA CGTCTTCGA AATGTGGATT CCAGAATGAT1560
 TGCTTAGGAA CTGACAAACAA AGCGGGGTTT TTAAGGGAAAC CCAGGTTGGG GAATAGGAGC1620
 TCTTAAATAA TGTGTCAAG TGCAATGGGG CCTCTGGGG GTTTCRAAGTT GAGGTTGATC1680
 TTGATCTACA ATTGTTGGGA AAAGGAAGCA ATGCAGACAC GAGAAGGGAGG GTCAGCCTT1740
 GCTGAGACAC TTCTTTTGT GTTACATCA TGCCAGGGGC TTCATTCAAGG GTGTCCTGTC1800
 TCTGACTGCA ATTTTTCTT TTTTGCAAT GCCACTCGAC TGCCCTTCATA AGCGTCCATA1860
 GGATATCTGA GGACATTCGA TCAAAAATAA GCCATAGACCA TGACACACAC CTCACTACCC1920
 CATTGAAGAC GCATCACCTA GTTAAACCTGC TGCGAGTTTT ACATGATAGA CTTGTTCCA1980
 GATTGACAG TCATCTTCA GTTATTCCTC TGTCACTTC AAACCTCCAGC TTGCCATAA2040
 GGATTAGGA CCAGAGTGCAC TGATATATAT ATATATTTTA ATTCAAGAGTT ACATACATAC2100
 AGCTTACCAT TTATATGAAA AAAGAAAAAAAT ATTCTTCCTC GGAAACTCACT TTTTATATAA2160
 TGTTTATAT ATATTTTTT TCCCTTCAAA TCAGACGATC AGACTAGAAC GAGAAATACT2220
 TTCTGTCCTA TTAAAATTAA TAAATTATTG GTCTTTACAA GACTTGGATA CATTACAGCA2280
 GACATGGAAA TATAATTTTA AAAAATTTCT CTCCAACCTC CTTCAAATTC AGTCACCACT2340
 GTTATATTAC CTTCCTCCAGG AACCCCTCAG TGCGGAAAGG TGCGATATTA GATTCTTG2400
 TATGCCAAAGT TTGTGTGAA AGCTGTGTC AGAGGAGAGG AGAGGAGAGG AAGGAGAAA2460
 CTGGATGATA ACTTACAGA ATTGAATCTA GASTCTTCCC CGAAAAGCCC AGAAACTTCT2520
 CTGCGATTC TGGCTTGTC ATCTGGCTCA AGGTGGCTGC TTCTTCCCCA GCCATGAGTC2580
 AGTTGGTGC CATGAATAAT ACACGGACCTG TTATTTCCAT GACTGCTTA CTGTATTTT2640
 AAGGTCAATA TACTGTACAT TTGATAATAA AATAATATTC TCCCCAAAAAA AAAAAAAAAA2700
 AAAAGAG 2706

(2) INFORMATION ON SEQ ID NO. 396:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2242 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

DRAFT DRAFT DRAFT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

CAGGCCGGTT CGGGCGAAGT TAAACCCCTCG GAGCTGGCCT CGGACTGCTG GGGCGTTACC 60
 CCTTCGGCCA CCCCCGCTGA CCATGGCAGT GTTTCATGAC GAGGTGGAAA TCAGGAGCTT 120
 CCAATATGAC GAGGACTCG AGACCTATT CTATCCCTGC CCATGTGGAG ATAACCTCTC 180
 CATCACCAAG GAAGATTCTG AGAAATGGGA AGACGTGGCA ACGTGTCTTA GCTGCTCTC 240
 CATTATAAAA GTGATTTATG ACAAAGATCA GTTTGTGTG GGAGAACAG TCCCAGCCCC 300
 TTCAGCCAAC AAAGAATTAG TAAATGCTG AAGAGCCTT CAGGAATCCA AATCTGAAC 360
 ATTTGGATG AGCCCAAGATA GAAATATCGA ATGCAAAGCT ACTGGCTTCA CAGAGACAAC 420
 CATTATATGAT TTGCTGTTCT GTAAAGAGTGT GGATTCTTC TATCAACTGC TGATCATRC 480
 TTCAGGAAGC AAGTCCATAA CATGACATAT CTGGATTTTG TGCTTAGAAC CTTAAATTGG 540
 AAGCATCTT AATTATGCT CTAATTTAA AAGAAGATAA TTCAAAACA GTGCTTCTT 600

TCCCTGGTT TCATCATTT CATATCTAA ACCAAATTAC TTGGTATCT GACAACAGCA 660
 TCATCTACCT CAGTCATTAG GATTCTTAA TAAAAAAGAG ATTGTATTT TGACTGTGTT 720
 ATTAAGATTA TAAAAATTAG CCCTCTTCTT GAAATATGAC ATCAGCTTTG CTGTTCTAA 780
 TTAAATTTA GTTGGCTTCAT CAGTACACCA CTTCAGCTTT CTATACCAAG CCAGTCTCCT 840
 CAGTTTCCC ATTAGAATGG ACATGTTCTG TTCAAGCTGT CATTCTGTA ATGCTCTCATO 900
 CAGAGAGTT GGTCTAGTA TTAAAGGAA AATACTGTA GGTCCACATG TCTCCAGAGC 960
 TAAAGCTTAG TGAAACAGAA AGAAAGCTCA AAATGAAGTG ATGAAAAGAT GAGGACTTT 1020
 CTTATATCT GCATATTCTC TTGGAGTCAG GACAAGATGA AAGAGAAAAC ATCCAAAAGA1080
 AGTGAATTG GTGACAGAAAT GAGAGGAGCA AAGCATACTA GTGTAGTAAG TGGAATGTT 1140
 GAATGACTTT GCCAGTCAG AGCAAGTAAT ATTCTGTAT CTGAGTTTTT GTTTGTGTT 1200
 TGTAAGGCT AATGAATATG CATTCCAGT AGGGGTTAAC GTCAARATTIC CATGGCTGGT 1260
 AGCTGGCTT TTGGCATATC ACAGTGTGTG GTCACTACTA CAAGGTAAAG CATCTACAGC 1320
 GGAGAATGAG CTGAAATAG AGAGACCTAT TTGTGATAAAA TATGCCCATG AGAGCATATT 1380
 TAATAAGCTT CTATAACATG CAGCCAAACCC AGACATCTAC TCCTGAGAG AAATGTTGCC 1440
 CTGGAGAAAAGAGATATAT AAAGATAGGC TATCACCCTT CTTTGCTGC AGTACTAAGC 1500
 ATAGCAAGAA ATTAGAATCA TTACATTGG AAATTGAAA ATTCCCTTTA TATACACAAAC 1560
 TTACTCTGT ATAATAAAAA AATATTATT AATGCACTGTA GTCCGTCAG GTTGTAGI 1620
 GAATGGCTT TGCAATTAGA AAAATAGCTT GTAGAATGT AAATGTTCTG CTACTGTTAA 1680
 ATGTAATGCA CACATTCTT GGACGTTAAA ACAAGTGAGT AGCCTTTTTT ACCTGCGAC 1740
 AGCATGGCTG TGTGCGCCA CTAGGCTGAG ACAATAATT ACCAAAAAATT ATAATGTTAC 1800
 GAGCTGAAAATGCTCAGTAC ATTATGTTGG ATTATCTGGA TGTGATGAGA AATCTCATGG 1860
 CCATTGGGA CACTGACATC CCAGAAGTAA TCCACAACTG CTTTGCAAAA GCAAGTGC 1920
 TGCTCAGATG AACAGAGCAG AGTACTCACT CACTATGGT GCATCAGCTG CAAAGCGAAA 1980
 TGAACGTCC CATGATCATG TTGATGGTTT TCTAGATACT GCAAACATGT TAGCTCTTC 2040
 TGATGCTGAT GAGTTCTAAA CACGAACAGA CANCCTGTAT GTGGGTTTGC TAAGAACATA 2100
 GAAGAACAGG AAGAAAAGTT GCCAGGGTTT AAAAATCCA GGGAAAAAAG AAGCATAAAA 2160
 AGCATTAGCA GTCAGTGAATGATGATAATG CTGCAATAA TGGGGAAATGG TTTGTTTTC 2220
 TAAACCCCAA AATTATTTT TT 2242

(2) INFORMATION ON SEQ ID NO. 397:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1239 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

TAGTCATCCT ACAAACATGT TTCTGTTACT TCCTAATATT AAAATAGCCA TTTTGGATTC 60
 CATATTTAA GTGCTCATTT GAGTGAATT CAAATTAGAA AGAAAATAT TAAAATGCGC 120
 CTAAACAAAA CCTCTCTTTC AGAATCCCTA TTCCCTGAAT CTTGGGTTTG AACTGCTTAT 180
 TAAAGGCAGG CCTAACATAA TTGTGAGAA ATGAGAAGT TTTAGTATAA ATTCTTTTA 240
 AAAATAATCA ATTACGGCTG GGTGCGGGGG CTCAGGCCTG TAATGCCAGC ACTTTGGAG 300

 GCCAAGGGGG GTGATCACCT GAGGTCAAGGA GTTCAAGACC AGCCTGGCCA ACATGGCAAA 360
 ACCCTGTCTC TACTAAAAAG TAAAAAAAT TAGCCGGCA TGTTGGCTTG TGTTGTAGT 420
 CCCACTTCAG TCTAACGTACG TGGGACTACA GGCACTGTGCC ACNAGGCCA GCTAATGTGG 480
 GTGTTTTGTT AGAGATGAGG TAGGGCCATA TTGCCCCAGGC TCGTCTTGAAC CACCGGGGCT 540
 CAAGGAATCT GCCCATCTTC GCCTCCAAA GTCTGAGAT AGCAGGTGTG AGTCANTCAT 600
 GCCCAGCCTC CTTGAAGTTT ACTAACATT GGGATAACTG AGGGAAGAGA AGTGACAATT 660
 CCACTCAGTC TATTAGAGGT CTGGATATAA GGTAGNCAC ACAATAACTC TAACNTTGCAC 720
 TTCTAACCAT TCTATCTTAT TGNNATTGGA GGCTGTCTTC TGNCAGATT TTTTGTGGCT 780
 TGAGATGATA TTTTNCGAAC CCTTCTTCA CTACCTTCT TACCCCTTAAT GTGNCCAAGC 840
 TTGAAACAGG ATTTGATTT CTGRGCNTAC TTGTTCNGCC TTCTGTGCGT CANCCAAGT 900
 ATCTGGTICA TCCTTNCCTN CTCATTCATG TTATTTCAA GTGAAACAAAG ACATTTGGG 960
 GGNNTCAAGTC TCNTTNGGN NTGTTTGTGTT TTATGTATA TAAAAATGGA TTGNTGTT1020
 CCCTTCCNA TGTAAGTAN CCAACTTATA TGAAAACCTCA CAATCATATA GTAAAAGAGA1080
 AATGAAANGC CTGGTGTATT GTACTTCAG ATGCCCTCCCT GNATGTATAG AATCNTCCTT1140
 GTAAAATAAA TAATTGNCAT TGATATCAG TCTTCCCCTA AATATTAATT ATTAAATATT1200
 TTAGAATTT TAAATACCAA CTATAAAAAA AAAAAAAA 1239

(2) INFORMATION ON SEQ ID NO. 398:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1663 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

GAACCTGCTC TCCTGCTTGC TGGTCCTTGT ACGCAGAGAC CGTTGCCTCC CCCACAGCCG 60
 TTGACTGAA GGCTGCTCTG GAGACCTAGA GTAAAACCGC TGATGGAAGT TGTGGGACCC 120
 ACTTCCATT CTTCACTGCA TTAGAGGTTG AAGGGAGGGG TCTCCAAGTT TGAGGATTGA 180
 GCAGATGAGG CTGGGGATC CCCCTGCTT GACTTCAGCC ATGGATGAGG AGTGGGATG 240
 CAGCAAGGTTG GCTCTGTGG CAGTGGAGTT GTGCCAGAAA ACAGTGCCCA GTTGTATGCC 300
 CTATAAGACA GGGTAAGGTC TGAAGAGCTG AGCCTGTAAT TCTGCTGTA TAATGATAGT 360
 GCTCAAGAAC TGCTCTGAGT TGTTGTACAG TGCCATGGCC AGCAAGAACCC CCAGATTCA 420
 GGTTTTATTA CAAAATGTA TGTTGCACTT GGGCATTTTG TAGTACATGG ATGAGTTAC 480
 TTTCCTCTT ATGTCCTGAGA ACTGTCAGAT TAAAACAGA TGGCAAAGAG ATCGTTAGAG 540
 TGCACAAACA AATCACTATC CCATTAGACA CATCRTCAAA AGCTTATTTT TATTCTTGCA 600
 CTGGAAAGAT CGTAAGTCAT CTGTTCTTGC ACCATGGCAC TGTCTGCTC CCAATGTTA 660
 GTGATTCCAA ATAATGGTTC TGTTAACACT TTGGCAGAAA ATGCCAGCTC AGATATTTTG 720
 AGATACTAA GATTATCTTT GGACATGTAC TGCGACTCTTG TGTCCTGTT TTGGATTACT 780
 GGAATACCCA TGGGCCCTCT CAAGAGTGTG GGACTTCTAG GACATTAAAGA TGATTGTCA 840
 TACATTAAC TTTCAATCTT CATTATGCAA TCTTGTGTTG AAATGTAACAC TTCTAAAAAT 900
 ATGGTTAACAC ACATTCAACC TTGTTTACCA AACTAAAG GAACCTCAGT GAATTGTTT 960

 TTATTTTTTA ACAAGATTTC TGAACTGAAT ATCATGAACCT ATGTTTTGAT ACCCCCTTTT 1020
 CACGTTGTC CAACGGAAATC GGGTGTGTA TATTCTCTCA TATGTTAAAG AGATGCTTCAT 1080
 AAATGTCAT TGCCTTAAAC TAAATTAACCT TCTCAAGAGA CCAAGGTACA TTACCTCTCAT 1140
 TGTGTATATA ATGTTTAAAT TTTGTCAGAG CATTCTCCAG GTTTGCAGTT TTATTTCTAT 1200
 AAAGTATGGG TATTATGTTG CTCAGTTACT CAAATGGTAC TGTTATTGTT ATATTGTCAT 1260
 CCCAAATAAC ATCGTCTGTCA CTTTCTGTT TCTGTATTGTT ATTGGTCAG GATTCTTAG 1320
 GCTTATTCAG TGTAATCTCT GCCTTTAAAG ATATGTCAG AAAATGTCAT TATAAATTTC 1380
 CATTGAAGTC GAATGATACT GAGAAGCTG TAAAGAGGG AAAAAGACAT AGCTGTGTT 1440
 TCCCCATAAG TTTTTTTAAAT TTGTATATTG TATTGTTAGT AAATTCCTAA AGAATGTA 1500
 ATAGGAAATAA GAAGAGTGTG GCTTATGTTA AGTCTCAACCA CTACAGTAGA AGAATGGAAG 1560
 CAGTGCACAAAT AAATTACAT TTTCCAAAAA AAAAAAAA AAAAAAAA AAAAAAGTGT 1620
 ATACGTTGGA ATGAAAAAAA AAAAAAAA AAAAAAAA AAAA 1663

(2) INFORMATION ON SEQ ID NO. 399:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2889 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

GATCAGGCCT GTGGTCCAGC TCACGTGCAT TGAGATTCTA GCTTGGGGCT TAAGRAATAT 60
 GAAAAACTTC CAGATGGCTT CTATCACATC CCCAGTCTT GTTGTGGAGT GTGGAGGAGA 120
 AAGGGTGGAA TCGGTGGTA TCAAAAACCT TAAGAAGACCA CCCAACTTTC CAAGTTCTGT 180
 TCTCTTCATG AAAGTGTCT TGCCCAAGGA GGAATTGTAC ATGCCCCAC TGGTGATCAA 240
 GGTCATCGAC CACAGGCACT TTGGGGGAA GCCTGTGTC GGCCAGTGC CAATCGAGGG 300
 CCTGGACCGC TTTCTGCTG ACCCTTATGC AGGGAAAGAG GACATCGTCC CACAGCTCAA 360
 AGCTCCCTG CTGTCCTGCC CACCATGCC GGACATCGTT ATCGAAATGG AAGACACCAA 420
 ACCATTACTG GCTCTTAAGC TGACAGAAAA GGAGGAAGAGA ATCGTGGACT GGTGGAGTAA 480
 ATTTGATGCT TCTCAGGGG AACATGAAAA ATGCGGACAG TATATTGAGA AAGGCTATTG 540
 CAAGCTCAAG ATATATAATT GTGAACTAGA AAATGTAGCA GAATTGGAGG GCCTGACAGA 600
 CTCTCTCAGAT ACCTTCAGAT TGACCGAGA CAAGTCGGAT GAAAATGAAG ATCCCTCTGT 660
 GGTTGGAGAG TTAAAGGGCT CCTTCGGAT CTACCCCTTG CGGTGTGACC CCAGGGTGCC 720
 AGCCCCCTCCC AGACAGTTTC GGGAAATTACC TGACAGCGTC CCACAGGAAT GCACGGTTAG 780
 GATTACATT GTTCGAGGCT TAGAGCTCCA GCCCCAGGAG AACAATGGCC TGTGTGACCC 840
 TTACATAAAA ATAACACTGG GCAAAAAAAGT CATTGAAGAC CGAGATCACT ACATTCACCA 900
 CACTCTCAAC CCAGCTTTG GCAGGATGTA CGAACGTGAGC TGCTACTTAC CTCAAGAAAA 960
 AGACCTGAAA ATTCTGCT ATGATTATGA CACCTTACCG GGGGATGAAA AAGTAGGGAGA 1020
 AACAAATTATT GATCTGGAAA ACCGATTCTT TTCCCGCTT GGGTCCCACT CGGGCATACCC 1080
 AGAGGAGTAC TGTGTTCTG GAGTCAATAC CTGGGGAGAT CAACTGAGAC CAAACACAGCT 1140
 GCTTCAAAAT GTGCCAGAT TCAAAAGCTT CCCACAAACCC ATCCCTTCGG AAGATGGGAG 1200

TAGAATCAGA TATGGAGGAC GAGACTACAG CTTGGATGAA TTTGAAGCCA ACAAAATCC1260
 GCACCCAGAC CTGGGGGCCCT CGTAAGAGGG GCTTGTCTT CACATCCTCA GGACTCAGG1320
 GCTGGTCCCT GAGCACGTGG AAACAAGGCAC TTTGCACAGC ACCTTCCAGC CCAACATTCC1380
 CCAGGGAAAAA CTTCAGATGT GGGTGATGTT TTTCCCGAAC AGTTGGGGC CACCAAGGCC1440
 TCCCTTCAC ATCACACCCCC GGAAAGCCAA GAAATCTACAC TGCGCTGTGA TCATCTGGAA1500
 CACCAAGGAC GTTATCTTGG ACAGGAAAAG CATCACAGGA GAGGAAATGA GTGACATCTA1560
 CGTCRAAGGC TGGATTCTCTG GCAATGAAGA AAACAACAGC AAAACAGATG TCCATTACAG1620
 ATCTTTGGAT GTGTGAAGGG ATTAAACTG GCGATTGTT TTCCCGTTTG ACTACCTTC1680
 AGCCGAACAA CTCGTATCC TTGCAAAAGA AGACCATTCG TGAGTATTG ACCAACCGGA1740
 ATTTGAAATC CCACCCAGGC TGATCATTCA GATATGGAC AATGCAAGT TTTCTCTGGAA1800
 TGACTCTTG GGTTCCTAG AACTTGACTG CGCTCACACU ATCAATTCTG CAAAATCACC1860
 AGAGAAAATGC AGGTTGGAC TGATTCGGC CCTTAAAGCC ATGAAACCCC TTAAAGGCAA1920
 GACAGCCTCC CTCTTGTAGC AGAAAGTCAT GAAAGGTGG TGCCCATGTT ACGCAGAGAA1980
 AGATGGCGCC CGCGTAATGG CTGGGAAGGT GGAGATGACAA TTGGAAATCC TCAACGAGAA2040
 GGAGGGCCGAC AGAGGCCAG CGGGGAAGGG CGGGGAGCAA CCCAACATGA ACCCCCAAGCT2100
 GGACTTACCA AATGACACAG AAACCTCTT CCTCTGTTT ACCAACCCAT GCAAGGACCAT2160
 GAAGTTCATC GTGTGGCGCC GCTTAAAGTG GGTCTATCATC GGCTTGCTGT TCCCTGCTTAT2220
 CCTGCTGCTC TTCTGGCCG TGCTCCTCA CTCTTGCGG AACTATTGT CAATGAAGAT2280
 TGAAAGCCA AATGTGTAAAC AAAGGCAAG AGCTTCATTG AAGAGTCATC CAGCAATGAG2340
 AGATACTTCG CTCGTAGAC CAACATTCAGC TGTTGATTGTT TGCTGAGAC CACACCCAG2400
 TAGCAGGTTA CGGCATGTCA CGGAGCCCCA TTGATTCCCA GAGGGTCTTA GTCTGGAAA2460
 GTCAAGGCAA CAAGCAACGT TTGCACTATG TTATCTCTTA AGTATTAAAAA GTTTTATTTT2520
 CTAAGGTATA AATCTGTGTT TTCAAAATAT TTTTCAAGGT GGCTGGTTCC ATTTAAAAAT2580
 CATCTTTTA TATGTGTCTT CGGTTCTAGA CTTCAGCTTT TGAAATATGC TAAATAGAAAT2640
 TCAAAATCTC CTGCACTTC AGGTGATATAA CTTCATATTAA GTAAATCACT GAAAGAGCTG2700
 TGCAATTATAA AATCAGTAG AATAGTGTAA ACAATTCTTA TTATGCCCA CAACCATTGC2760
 TATATTGGT ATGGATGTCA TAAAAGCTTA TTAAACCTCT GTATGAAAC TAAATAAAAAA2820
 TGTTTCAACCT TTAAACACATA GGGGGGGTGG TCGGGGGGTC GGGAGGGGGG GGGGTGGTGT2880
 GGGGTGTGG 2889

(2) INFORMATION ON SEQ ID NO. 400:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1774 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

TGAAAGGAAGT AACAAAAGTG GGAACCCCT GATAAACCCC CTCAGGATCC TCATGGAGAA 60
 CTTACCTATC CAGGAGAAT AGCAAGGGG AAAGAACTGG CCCCCCCCTG ATTCCGATGA 120
 CCCTCCCCCC GGGTCCCCCTC CCCACAACAT GTGGGAATTC CCAGAAGATA AATTCAAGTT 180

GCAATTTCAG TGGGGACATA GCCCAAACCC ATATCACTGG TGATGCCAAC TTCTTCAGTA 240
 TTAGGGATTC TCAGTCAGAA GAGACCCCTT GTGTGGCTCT AGTCCCCCTCA GGAGGAAGT 300
 GGACAAACAGA GAAATGAGAG TTTTGATATT TTCTGAAAAGA GGAAACATGTG TTAGAGATGA 360
 AGAATCTTC AAGGGTCATG CAGTTGCTTA GAATAATCAT TACTGTTATA TGAGAAAACAT 420
 TTAGTAATT ATAATAAAGG ATAATGTTA TTTAAAAAAC CTGACTTTTC CAGAGTAATT 480
 TTGTTTGCATG CATTGATGTT TATTGAACTG GACTAATTTC TATAATGCAA ATCAGAGTTA 540
 AATATTAAGG ATTTGTGTTAA TACAATGAC ATAGGAATTCA CATTAAAGATA TTAGGAAGAA 600
 ACRAAGGACAA ATTAGACACT TGAATCGGA GAGATAAAGC TTACTTGACT TTCAAATGGA 660
 GAGATGATGA AAACCCACTC ATTCACTGT TTCAAGACAAA AAGACAGCTCA TCTGATAAGA 720
 GTATGATCATG GATGATGATGC CCTCACAGGGG CCTTGGACAT CTTTAAATTTC TGCGATTTCG 780
 TGRAAGAGGT GGACTTTCAG GATAATGGAG CAGAACCCAA CATTAGTAAAGGAAATCCC 840
 ACTTCTCCC ATAGAATTAG AAACATGTGA AAGTACAATA AACTTCTGT TCAAATTAC 900
 AGCATCAGAG AGCTTCCCCT TTGCACTCATG ACCTTGAATT TATATTATTGAT GATCAAGTTC 960
 TAATTTGTAT GTATATTTCG TGCAATTACA CCAATAACAG TTAAAATTAA TTATGTGTTA1020
 TAGTTAATAT ATGCACCTAC CTTCTTCGCT TAGTGCACTCA GTAAATGTGT TATTTTGTC1080
 TTTTCCAAA GAGAGTTGAG TAGGTTTCC TGCTAGTTCT TCCCTTATAG CTTTTCTCTT1140
 GATAACCATC ACTTCAGGAG CTTTAAACAT ATCTATCTTG CATTGTTGTC TGCGGGAGAA1200
 CTAGCCATCA GCCTCTGAA GCCTGCATC ATTGTAAATT TGAGGACTGG GCTGTCCTGG1260
 GCTCAGAG GTAAGAAGACT ATTGAGCTTG ATGTGTGTTG GTGGCAGTGG ATTCCACCCA1320
 ACTGCCAAGT TAGTTTGTG AGAGATTCA TTTTACACAA CAAAAATAAG CCTGTGCA1380
 AGATTTTAAAT ATCATGGAA GTTAAATCT AGAAAGACCT TAGAGAAACCA GCAAACCAAC1440
 TCTCTCATTT AAAAGTGAAG GATTCTAG CACAGATTAC TTGCTARGA TCATCCAGGA1500
 CGGAAGACAA GATCTCAAAT GTACTGGGG ACAAGAATTG GTCCCCAAT TCAGTGTCT1560
 TCCTAGTATT AAACATGCG CCTTGGACA ATTTTGGAT TTCAAATCTG GTATATTTC1620
 GTAACCTGC TGATTTTATA GTTGTACTGGG TAGATGACAT TAGAATGTAG ATAGGTGCA1680
 CGCTATGATA GACTCTGCTA AGACATGTC CCAGTGTCCA GCAGCAATGT AGATATGTGT1740
 GACAGTGGTC ATGTAGAAGT TATAAAGCAG AGTA 1774

(2) INFORMATION ON SEQ ID NO. 401:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3982 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

CCCAAGTGTG ATGCATTGTT CTTCAGATGT TGAAAAGAAA GCAAAAAATA CCTCTTAAC 60
 TAAGACAGAA TTTCACAA AATGAGCAGT AAAAGTCACA TGAAACACTC CAAAATCAGT 120
 GCATTTGCA TATTTTAAA CAAAGACAGC TTGTGAATA CTGAGAAAGAG GAGTGCAGG 180
 AGAAGCTG TACTAACAAA GCCAAATTC TCAAGCTCTT ACTGGACTCA GTTCAGAGTG 240
 GTGGGCCATT AACCCCAACA TGGAAATTTT CCATATAAT CTCATGAAT TCCCTTCAT 300

 TTGAATAGGC AAACCCAAAT CCATGCAAGT GTTTTAAAGC ACTGTCCGTG CTTAATCTTA 360
 CATGCTGAAA GTCTTCATGG TGATATGAC TATATTCACTG ATAGCTATGT TTTCTCTT 420
 CTCTGTAAAGA ACTGTGCGAT GATCCAACCTT CAGCAATGAA TTGTCCTAG TGAGAGAACCT 480
 CTATAGATCT TAAAAAAATGA ATTATTCTT AGCAGTGTAT TACTCACATG GGTGCAATCT 540
 TTAGCCCCAG GGAGGTCAT AATGTCCTT AAAGGCAGAA GTCACATTT ACCAATATGC 600
 ATTATCATCA ATTGTGCTGTT AGGCTGTATA TTCAAGCTGTG TTGTCCTTAAC ATTTTGATA 660
 AAAAGAACAA ACAGAACATTA TCTGTCATT GAGAAGTGGC TTGACAATCA TTGAGCTTT 720
 GAAGCAGTCA CTGGGTGTA ATATGAATGC TGTCTAGTG GTCATAGTAC CAAGGGCAGC 780
 TGTCTCCCTG TGGTATAACT GATTTCTTT TTAGTCCTCTG ACTGCTAAAT AAGTTAATT 840
 TGCTATTTGC AAGAAAGAAC ATTGATTGCT AAATCTTTT GCTGCTGTGTT TTGAGCTTT 900
 TCATGTTTAC TTGTTTTATA TTGACTGTT TAAGTATGAG AGGCTTATAG TGCCCTCAT 960
 TGTAATTCGA TAGTGTCTT TTGAGCTTAA TTGAGCTTTA GAAAGTAGCT ATGTTGTTAA1020
 CAGAGGTGAT GGCAGCCCTT CCTTACACAA CTGGTGGAG AGACCCCTTA AGAACCTGAC1080
 CCCAGTGAAT GAAGCTGTGAT CACAGGGAGC ACCRAAGGAC CTTCGTTAAG TGATAATTG1140
 CCTGGCCCTG CAGCCATGAC CGTTAGGAA AAATATCCC CATTGCAACT TARACAGATGC1200
 CCTCTCTCCA AAGAGAATTA AAATCTGAGC TTGTCAGAT CAAGAGAATA TACTGGCAG1260
 AATAGGATAT GTTGTGTTAT TTGTTCTTAA AAATTAAGGA TTGAGCTTAACT CTGGAGAGTA1320
 AGATATAGTA TAGGTTTGC CTCACACAT GTGAGGGCCA AATAACCTGC TAGCTAGGCA1380
 GTAATAAACCT CTGTTACAGA AGAGAAAAAG GGCGGGCAGC AGTGGCTTAT TCTGTAAAT1440
 CCAACACTGT GGAAGGCCGA GGCAAGGGAGA TCACTTGAGT CCAGGAGTTT GAAACCTACC1500
 TAGGCAACAT GGTGAAACCT TGTCCTTACCA AAAATAAAAA TTACGCTGGC ATGGTGGCAC1560
 GTGCCGTGTT TCCCAGCTAC TTGGGAGGCT GAGGGTGGAG CCTGGGAGGT CAAGGCTGCA1620
 GTGAGCCATG ATCATGCCAC TGCACTCCAT CCTGGGTGAC AGCAAGATCT GTAAAAAAAA1680
 AAAAAAAAGA AAACCCAGGAG TGAAAAGGA AAGTAGAAGG CAGCTGCTGG CCTAGATGTT1740
 GGTTGGGAA TATTAGGTGA TCCCTGTTGAG ATTCGCTTAC CAGAGCAATT TCTTTAGCTT1800
 TTGACTTTGC CAAAGTGTAG ATAGCCTTAA TCCAGCAGTA TTGAAAGTGG GGAATGCAAC1860
 GTGAGGCCAA CTGACAAATT CCCCCCGTGG CTGCCAGAT AGTCACAGTC AAGGTTGGAG1920
 AGTCTCCCTTC CAGCCAGTGA CCTACCCAAA CCTTTGTTTC TGAAAAGCTG CTCTGGAAAT1980
 ACCGGGAAGC CCAGTTTCTC CACGTGGTTT CTAGCTTCTT CAGACTCAGC CCAAATTAGG2040
 AAGTGCAGAA GCACATGATG GTGAAAACC TAGGATTGG CAGCCTTCGA GAATGCTATG2100

GAATCTGAGG GAAGATTTAT GTTCGTTT GGAGGATAGC TCAAGTCAA
 AGCCAGTAC CCTTCAACC TACCCATACT TTGTACAACT CTTACACAAA TACTTAGATA2220
 TTATTAGAT AGCCCTGAAT TCACCTAAT TATAAACAGG GAGTGTAAAC TGCCCCCAGA2280
 TGTCCCTGGG CTGGTAAAAA GCAGCTGGAG TGAAAGCACT ATTTCCTCATA AAGGTAAACAA2340
 AGGGCAGCTC AGTGGTTACT CAAGCTCAAAG AGGGTTTTTA TAAGAGCAAG CATTGGTTAA2400
 GTCTGTGAT ACTGAGTTGG AAATGATTTC AGCACATTCT TTTTAGTGG AGTGAAGTT2460
 CTAAAGCCCC CTTTAACTT CCTCTTGGT TTTCATTATA ATTGGTAGGC ATCTCATGAA2520
 CTGTCTCTGA CTGTTGTCCTC TTGGTGGTCA TGAGTGGTG AGCTTGCTTT CTGACTTGCA2580
 TTTCTGACTT TATCCTGTG TAGGAAGAT AGAAACTAGG TTTGAAAGA TTACATGATT2640
 CAAGCGAGGG ATTCTTAAAGT AAAGATGTAT TTATCTGAA GAATCTAAA GATAACAGAT2700
 TATTTGCTTA TGAAGAACAA ATATAGTCCTA GGAAATCCAG AATGTCAGC CAAAGGTCATA2760
 AGAAAGTCATC TCCTTCAATC ACTTTAAATAA AGAAAGTATT CGAGGGAGATA TCTGTCAA2820
 AAAGTTTGAC TGGCCCTCAG ATTCCAGTT TTTTTAAAAA GCAACTTACCA ACTAAATCCT2880
 TGAGTCTCCA TAGAGTAAAC GTAAAGAACAG TGATGTAAAC GACTCTCCCTC TCAAAGGATC2940
 TCTCTGGAA GAGACTATCA GCGGCAGGAT TCTCCAGGAG AGACCCATCC CCTAGTGCAC3000
 GAGCTTGCAT CCTGGAGACT AAAGATGCA CTTTTTGTA GTTTTTGTC CAAATGCAAT3060
 CCCATTCTG TGCTCTTAG CATGCACTA GATTGGACAA ACAAGGATTC CTAAGGAATG3120
 ACTTTTAAATCA CTATAATATG GTTACACGTA TTATATAAAAT ATATATTCTG TTATAGTTC3180
 TAATATGGAG ATGTTGTTG CAATGCTGGC CTGTTGGTGGT CTGTTGTAATG CTTAACTTGT3240
 TATGGAGGAG GCCAGGCTCA GAGCTGAGAT GTGGCCCTGAA CCTTCCCTGT ATCGATCCTT3300
 TAATTAGAA CTGTCAGAT GTCACTTCT CCCCTCTGCG CTTTTAGTGG TATCTGACAT3360
 ATACTCAAAA CAGTAATTTC CTGGTCACAT CTTAACTGCA TAATTCTGTA TTATATAAGA3420
 ATTTTCRCAAT GGRCATGTAC AAATTGACAC TCAAAACCATC CCCRAGTCCAG ATACAGGGCA3480
 GCGTGTAGGT GACCACACCA GAGGCCCTAGC CTGGTCCCTT CTAGCGCTC GGGATGGAT3540
 CCAGGCATT CTTTAAATC TCAGAGGTAG CAGTAAACATT TTCACTTATG CTGTTAGCAA3600
 GTGTGTGTTT GCAAAATAGAT ACCCATTATA CTAAATGTCCTC AAGTAATGT TCATTCACAC3660
 TCTGCTCCA CTGTTGTCCTC ACGGGTGCA TGAAAGTGTG GAGGAGCCCG TCATCTGGAG3720
 GGATGAGTGC TGCGTTGACT ACTGCTATCA GGATTGTTGT GTGTGGAATA TTCACTAC3780
 TAAATTATAT ATGCACAGTA ATTCCCTTT TTATATGTCAGA AGTAACATT TGTAAAAGT3840
 ATACTCACAA ATTATTATAA TGATTACTAA TATATTTTT CCATGTTCA TTGCCTGAAT3900
 AAAAAGTGT TACCACTGTT AAAAAAAAAA AAAAAAAAAA AAAAAAAATGG GAAAAAAAAG3960
 CTGGGGGGGGG GGCCCGGTAG CC

(2) INFORMATION ON SEQ ID NO. 402:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1876 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

CTCTGGATC	CCCTGGACCA	CTGGGCATAC	TCGCCATCCT	CTTCCGGAGA	TCTGGGCA GT	60
TCGCTGCAT	TAGAGCTCT	GATTGAGATT	CAGTGCATCA	GGCGTCTAT	CCATCACGTC	120
CACACCTCTG	TGCCCACTCT	TGAAGCTGTT	GGAAATATT	CAGCAATGTC	CCGATCAACT	180
TGCAAGAGAA	TATAAAATGAC	ATTTCGAAGG	TAGAAAGATAC	CTGATTTTTT	TTCCTTTAA	240
TTTCTCTGGT	GCCAATTTCA	AGTTCGAAGT	TGCTTAATACA	GGAAACATT	ATGAATTGAA	300
TTATCTTGT	TGAAAATAAA	AAGATCACTT	TCTCAGTTT	CATAAGTATT	ATGTCTCTTC	360
TGAGCTATT	CATCTTTT	TGGCAGTCTG	AATTTTAAA	ACCCATTAA	ATTTTTTCC	420
TTACCTTTT	ATTTCGATG	TGCAACCA	TGCTTTATT	GGCTGAGATA	TGAACATATT	480
GTTGAAAGGT	AATTGAGAG	AAATATGAG	AACTGAGGAG	GA AAAAAG	AAAAGAGAAA	540
GAACCAACAA	CCTCAACTGC	CTACTC AAAA	ATCTTGTC	TTTTATGTTA	ACGGAAAGAA	600
TCCAGGGTAT	GGCCATGGAG	TGTACAAAGT	TTGGGCGAGA	TTTCAGCAA	ACTCTTTCC	660
CACTGTTTAA	GGGATTTAGT	GATTACTGCC	ATTCACTTC	TAATTCAGTA	GGATCCAGTG	720
ATCTTACAA	GTTAGAACAC	AAATATCTCT	GGCTTCTCAT	GATCCA ACTA	ATGCCCTACT	780
CTTCTTGAAA	TTTTAACCTA	TGATATTTTC	TGTGCCTGAA	TATTGTTAT	GTAGATAACA	840
AGACCTCAGT	GCCTCCCTGT	TTTCACATT	TTCCCTTCA	AA TAGGGGT	TAATCAGCAG	900
CTCGCTT T	GTCA GAGGCC	TCCCTGAAAGA	CCAAAATAG	AAATATCCAT	ACCTAGTTT	960
CCATGGGTGT	TTCTGACTCT	GAGCTACAGA	GTCTGGTGA	GTCCTCTCT	GGGCTTCATC	1020
TGGCAACAT	TTTATCGTGA	GTGGGATGG	TTGACACTAG	CCCAATGAAA	TGAATTAAAG	1080
TGGACCAATA	GGGCTGAGCT	CTCTGTGGC	TGGCAGCTCT	GGAGG CAGC	TTTCCC TGCC	1140
TCTCTACAA	TGAATGAGGT	CAGCACTGTC	ATTCACTCTC	GTTTATTTTC	AA GAATTAATC	1200
ACGCTTCTC	GAATCCAAC	TAATCCATCA	CCGGGGTGT	TTAGTGCTC	AA CATGTGT	1260
TCCCATTTCA	GCTGATCAGT	GGGCTCCAA	GGAGGGCTG	TAAAATGGAG	GCCATTGTGT	1320
GAGGCTATCA	GAGTTGCTGC	AAACCTGACC	CTGCTCAGT	AAAGCAGTTC	CAACCGTCTG	1380
TTATGCTGT	ACACATGGCC	CCTCCCCCTG	CCAGGAGCTT	TGGACCTAAT	CCAA GCA TCC	1440
CTTGGCCAG	AAAGAAGATG	GGGGAGGAGG	CAGTAATAA	AA GATTGAA	TATTTTGCTG	1500
GAATTAAGTT	GGAAATTCTCT	GAACCTAAC	TGAGGAAATT	CACCTGTAAA	CTTGAGTCTG	1560
ACAGAAAAGCT	GCCTGGTATA	TCCAAAAGT	TTTATCTCT	CTGCTCATA	TGTGATTC	1620
GCCTTTGGGG	ACTTTCTTA	AA CCTTCA GT	TTATGTTTT	TTTCA TACA	CTTATGGAA	1680
CTCTGCTG	TTTGGCCTC	TTCCAGCTT	CTGACACTT	TAATTACAA	CCTGTTACCT	1740
ACTTGTACTT	TTTGCA TT	AAACAGGACA	CGGGCAGGG	AGAAAAGGT	TTAGTTT	1800
AAACCCGGTG	GTTACCA TAA	CGCGGAAAA	GGTGGCCCAT	ACGGGGC	CGTTTTGAA	1860
AGGTTAAGGG	TATTTT					1876

(2) INFORMATION ON SEQ ID NO. 403:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1216 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

TCTGTTCTGT GGCAAACTGT TACTGTTCTT CGGTGGCCRA CCATGGCGGC CACCAAGCCCT 60
 ACCCCCCCTC CGGGCACTTT CCTGGACAG TGCCCTCGCA GGAGTACTCA CACCCGCTCC 120
 CGGCCACACCC CTCCGTCCCC CAGTCCTTC CAAGGCTGGC GGTCAAGACAG TGGCTTGAGC 180
 CCTCCCAAGCA CGGGGGCACAC CAGGATTTC ACAGGGTGTCA TGGGCAGCCG TCCACCAAAC 240
 ACTACGTGAC GAGCTAACCG CAGCGAGGG CGGGGGCGGT GGGGAATCTT CCTCCCCAGC 300
 CCCCGGCTC GGGAGTTATG CATCCAGAGA CCTGCCCTTC TACCTTCCTTC GCCTCCCCCTC 360
 TTCTCATTC CATTGGCCCA GGCTTTTCCC TTTTGATTAT GTGTTTGGTT TTGGCTTTG 420
 TTTTGATTTC TTGTTTATAT GAATCTCTCG GAGCGAGAGG TGACAGTGGG AGCTGGCCCTG 480
 GGCCAGGACG GCAGGTGGCC CTGGAGATGG GAAAGTGTCT GTGTCGAGGC GCTGAGCTCT 540
 CTCTCTGTTC CTCTTTTTTC CTCTACTTCC TTCCCTCTCA CACCCCCGTTG GCTGAAAGGA 600
 ACCTCGCTT CCTGTAAAGC TTGGGGTCTT CACCCCTCTT ACCCCACCCG GGAGGAACCC 660
 CCAGGGCCCC GGGCTTGTTC CTCTCTTGT TTTCCTTTG GCCAGTTTG TAATGTATGG 720
 AGTAAGGAAT GACCTTTAGA TTGTGGGACT TTGTGTTTG TTTTTTTAAA TTTTTTTAAA 780
 CCAAGAATGA TTCTCTTGC TTCTCTTCC TCACCATCTT CCCAGACGGG GTTCAAAGGC 840
 CACTTCTCAA GCAGCTTTTG GCACCTTCAG CCTCAGAGTG AAATTTTTA AAGACAGGAC 900
 CCCTATGTCC AGGAAAGGG AAAAGGAACCT TTGCCAATGAG TAGTGACCCRAC AGCAAAAGGA 960
 ATAAAAATAAT AAAATAAAAAC AATATGACAC AGCCCTTGTG GAGGTCAAGCA GGAGGAGGG 1020
 GCTGCCCGGA GTTGGGTCTT TGCTGGATT TTGACACAGC AACTTCCTGT AGTGAGCAGT 1080
 TTGTATGAT CGTGGACTTC CTGTTCTCAA GGCGCAGGTG TTATTTCTGT ATCTGTCTAG 1140
 AGCACACACC AAAATCCAAC CTCTAATAA ACATGATGGC GCAGTCCRAA AAAAAAGAAA 1200
 CAGAAGAAGA AAAGGG 1216

(2) INFORMATION ON SEQ ID NO. 404:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 271 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

RPRAGASIST LAGLSLKEGE DQKEIKIEPA QAVDEVEPLP EDYYTRPVNL TEVTLQQQL 60
 LQPDFQPVCA SQLYPRHKHL LIKRSLRCRK CEHNLSKPEF NPTSIKFQIQ LVAVNYIPEV120
 RIMSIPLNRY MKESQVLLTL TNPVENLTHV TLFECEEQDP DDINSTAKVV VPPKELVLAG180
 KDAAAEYDEL AEPQDFQDDP DIIAFRKANK VGIFIKVTPQ REEGEVTVCF KMKHDFKNLA240
 APIRPIEESD QGTEVIWLTQ HVELSLGPLL P 271

(2) INFORMATION ON SEQ ID NO. 405:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

DLKQDQGKQK ICIFLKSLGH LLTILLQKTR CSWWSTLSSF ILENIEEIKV SNPTPGYQVK 60
 TASLLLQNC GLLAELFYGL QSKWSYLTHH MTKVNLVRG KVLDIQFWIQ EIIIIVNFPFK120
 SMERMLVENI LKI 133

(2) INFORMATION ON SEQ ID NO. 406:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

RGPGHLLKPN GGPPMKGYGYG RNLDISPLP LNRETVKRSL RFHRFWPLIP NSFPHNNSVFL60
 VSMKCLESR KPVKIFLKKK KPQKTDHSI QWTSI 95

(2) INFORMATION ON SEQ ID NO. 407:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

YLSLCPCWPG NFFQWCLLEE VFSSCHFKKI KLEIEYGWHD CTLLVLLFFY SSVPL 55

(2) INFORMATION ON SEQ ID NO. 408:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

LQEAPCGEHG RHLHKSAMRR DTESELHHQR QVQGAETVGS GQGSAAFSGP SPYARGPGPD 60
 LPLLGGQHLS IRRWFCKVTM SQCVLELPFS NANLPSLHIS PHPWTRFCVS ESGNLLKRGG120
 STPGLLV 127

(2) INFORMATION ON SEQ ID NO. 409:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 95 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

KGVGLLIMGG QQQVLGHRRER VRRMLQTPAH CPRSPLPAPA SDGAALIPCL SSLQIYEGAY60
 HVLKHKELPEV TNSVFHEINM WVSQRTATAG TASPP 95

(2) INFORMATION ON SEQ ID NO. 410:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 296 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

VVRLAPTFGH YVCTVISHAH EVRQMQUELR VRSGVMSEKD HMVTMHDVLD AQWLYDNHKD 60
 ESYLRVVVYP LEKLLTSHKR LVMKDSAVNA ICYGAKIMLP GVLRYEDGIE VNQEIVVITT120
 KGEAIACMAIA LMTTAVISTC DHGIVAKKIR VIMERDTYPR KWGLGPKASQ KKLMIKQGLL180
 DKHKGPTDST PATWKQEYVD YESASAKKEVVA AEVVKAPOVV AEAAKTAKGS EESESSESDET240
 PPAAPQLIKK EKKKSKKDKK AKAGLESGAE PGDGDSDTTK KKKKKKAKE VELVSE 296

(2) INFORMATION ON SEQ ID NO. 411:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 280 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

RDQGGGSLRS FPRLWTGRHD AVQGNMADAE VIILPKHHKK KKERKSLPPE DVAEIQHAE 60
 FFIKPKESVK KADTSQLWLL LKNFDKLNVR TTHTYPLACG SNPLKREIGD YIRTGFINLD120
 KPSNPPSHEV VAWIRRLRV EKTHGSGTLD PKVTGLIVC IERATRLVKS QQSAGKEYVG180
 IYVRLHNAIEG GTQLSRALET LTGALEFQRPP LIAAVKRQLR VRTIYESKMI EYDPERRLG1240
 FWVSCEAGTY IRTLCVHSQD SRARGTSDAQ ASEGSFWSH 280

(2) INFORMATION ON SEQ ID NO. 412:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

RPHPHPEGVMG FSRGCGSASS ILWKPDHCPW QRFPGHQEFE EERLRPAGMH GTQRGRGGQV 60
 DPAAHCPGAH GETHLPRPDQ REDHGHHGAT TFSLNCSAAG TTPPSLWVWL PNGTDLQSGQ120
 QLQRFYHKAD GMLHISGLSS VDAGAYRCVA RNAAGHTERL VSLKVGLKPE ANKQYHNLVS180
 IINGETLKL PCTPPGAGQGR FSWTLPGNMH LEGPQTLGRV SLLDNGTLTV REASVFDRGT240
 YVCRMETEYG PSVTSIPVIV IAYPPRITSE PTFVVIYTRPG NTVKLNCMAM GIPKADITWE300
 LPDKSHLKG VQARLYGNRF LHPQGSLTIQ HATQRDAGFY KCMAKNILGS DSKTTYIHVF360

(2) INFORMATION ON SEQ ID NO. 413:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 314 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

EEGDYTCFAE NQVGKDEMRV RVKVVTAPAT IRNKTYLAVQ VPYGDDVVTVVA CEAKGEPMPK 60
 VTWLSPTNKV IPTSSEKYQI YQDGTLIQQK AQRSDSGNYT CLVRNSAGED RKTWIRHVNVL20
 QPPKINGNPN PITTVREIAA GGSRKLIICK AEGIPTPRLV WAFFPEGVVL P APYYGNRITV180
 HGNGSLDIRS LRKSDSVQLV CMARNEGGEA RLILQLTVLE PMEKPIFHDP ISEKITAMAG240
 HQHSASTALP RGPRHHPAWCG SFFMAPICRV DSSCSASTR LTACYTLAVS PRWTLGPTAA300
 WPAMPLATTR GWSP

314

(2) INFORMATION ON SEQ ID NO. 414:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

RPVPAKLNPR SWPRTAGALP LRFPPLTMAV FHDEVEIEDF QYDEDSETYF YPCPCGDNFS 60
 ITKEDLENGE DVATCPSCSL IIKVIYDKDQ FVCGETVPAP SANKELVKC

109

(2) INFORMATION ON SEQ ID NO. 415:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

YAKSTATSHG NLTLTPTWNA ISLALSCHKQ KLYRNRNITCS DLAKSFKHST YYTGMLCSSH 60
 SVTNTTSFGC FSFHLVLTSK EYAEYKKSPH SFITSEWTFF LVH 103

(2) INFORMATION ON SEQ ID NO. 416:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

YTMKIIYFTR KILYXQGGIL KYNTPGSFL LYIMIVSFHI SWXLXXGKGT XKSIFIYIKT 60
 KXXQXRLKPP KCLVSLENNMM NEXXXKMNQIT WXTTHRRXNKX AQEIKSCFKL GHIKGKKGSE120
 RRVRKISSQA TKNLXRRQPP NXIR 144

(2) INFORMATION ON SEQ ID NO. 417:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

LILMGRLIYN XNYLFYKXDS IHXGRHLEVQ YTRKFISSLR YDCEFPYKLX TXHKKGNXXKI60
 HFYIHKNKTX PXET 74

(2) INFORMATION ON SEQ ID NO. 418:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

YPFFTLQRN RVFDIISYYVK EMLQNVNCFK LKLPLKRPRY IYLIVYIMFN ICQSILQVCS 60
 FISIKYGYVV AQLLKWYCV YICTPNNIVC TFCFLYCICA GFFRLYQCNL CLLRYVQKMSI120
 I 121

(2) INFORMATION ON SEQ ID NO. 419:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

FFFFFFFSS FQRIHFFFFF FFFFFGKNVI YLHCFSHSSTV VLGLNISITL LFPIYILLEY 60
 YYKYNIQEKK TYGETQLMFF SPLYRLLSII RLQWKFIWTF SVHILKGRDY TDKA 114

(2) INFORMATION ON SEQ ID NO. 420:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 765 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

IRPVVQLTAI EILAWGLRNM KNFQMASITS PSLVVECGGE RVESVVVIKNL KXTPNFFSSV 60
 LFMKFVLFKE ELYMPLVIK VDHRQFGRK PVVGQCTIER LDRFRDCPYA GKEDIVPQLK120
 ASLLSAPPKR DIVIEMEDETK PLLASKLTER EEEIVDWWSK FDASSGEHEK CGQYIQKGYS180
 KLKIYFNCELE NVAEFEGLDTK FSDFKLYRQ KSDENEDPSV VGEFKGSFRJ YPLPDDPSV240
 APPRQFRELP DSVPECTVR YIIVRGLELQ PQDNNGLCDP YIKITLGKKV IEDRDHYIPN300
 TLNPVFGRMVY ELSCLYLPQEK DLKISVYDYD TFTREDEKVGE TIIDLENRFL SRFGSHCGIP360
 EYCYVSGVNNT WRDQLRFTQI LQNVARFKGK PQFILSEDGS RIRYGGRDYS LDEFEAANKIL420
 HQHLGAPEER LALHILRTQG LVPEHVEVTRT LHSTFQPNIIS QGKLQMWWDV FPKSLGPBP480
 PFNITPRKAK KYYLRVIIWN TKDVLDEKS ITGEEMSIDIY VKGWIPGNEE NKQKTDVHYR540
 SLDEGEGNFNW REVFPFDIYQ AEQLCIVAKE EHFWSIDQTE FRIPPRLIQ IWNDNKFSDL600
 DYLGFLELDL RHTIIPAKSP EKCRRLNDIMP LKAMNPLKAK TASLFEQKSM KGWWPCYAEK660
 DGARVMAGKV EMTLLEILNEK EADERPAGKG RDEPNMNPKL DLPNRPETSF LWFTNPCKTM720
 KFIIVWRRFKW VIIGLFLILLI LLLFVAVLLY SLPNLYLSMKI VKPNV 765

(2) INFORMATION ON SEQ ID NO. 421:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 289 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

ETQVVIQRKL VIVPYLNDQP GWDSKFRLLVN TPEMLLFRND TELFGWKVKV RENKSPVKIP 60
 FTIQRSVMDI CFEVFFIAR NPADFVDVTH FLSCDAFLVQ DNVLGVPPDDH TQVVFGLFPG120
 CDVERRAWWP QTLEGENIHPH LKFSLGNVGL EGAVQSPCFH VL RDQFLSPE DVKS KPLFRG180
 PEVLVQDFVG FKFIQAVVSS SISDSTPIFG KDGLWEAFES GDILKQLCWS QLISPGIDS R240
 NTVLLWYAAV GPKAGKESVF QINNCFSYFF IPGKGVIIID RNPFQVFFL 289

(2) INFORMATION ON SEQ ID NO. 422:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

FFLYSFSSDN HDFRSFKTIY LAFVSGGELA ISLLKPAIIV NLRTGLSWGS EGKELFEQMC60
 VGGTGFHPTA KLVILLEISFY NTKISLCQRF 90

(2) INFORMATION ON SEQ ID NO. 423:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

TPSGSSWRTY LSRRNSKGGER TGPPLIPMTL PPGPLPTTCG NSQKINSSCN FSGDIAQTHI60
 TGDAHFFSIR DSQSEETPCV A 81

(2) INFORMATION ON SEQ ID NO. 424:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

ENWASRYFQSFTEQKVWVG HWLEGDSPTL TVTIWAATGG IVQLASRCIP HLKYCWIKAI 60
 YTLAKSKAKE IALDPESQQD HLIFPNQHLG QQLPSTFLH SWFFFFFFLQ DLAVTQDGVQ120
 WHDHGSLQP 129

(2) INFORMATION ON SEQ ID NO. 425:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 122 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

EAQKWDClWT KNYKKVQSLV SRMQALALGD GSSLLENPAAD SLFQRRSFER RVCYISFFTVA 60,
 TLWRLKDLVV SCFLKITGIW RPVKPFWTDI SSKYFFIKVF EGDDFLDLWL DILGFPDYIV120
 LS 122

(2) INFORMATION ON SEQ ID NO. 426:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 105 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

RFKKSPQRQN HNMSRRNKKL LDIPGSFLYD SGLQVKFLSL SSEEFLIPKA KYFNLFITAS 60
 SPIFFLGKGM LGLGPKLLAG GGAMCHSITD GCKCFTEQGS GLQQL 105

(2) INFORMATION ON SEQ ID NO. 427:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

EKEYELRRKK KKKKRTNNLN CLLQNVGAFM LRREEFQGMAM ECTSMWADFQ QTLFPLFKEL60
 VDYCHSLHNP VGSSDPYKLE NIIFCLLMIQ LMPYSS 96

(2) INFORMATION ON SEQ ID NO. 428:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

RKKGETEREL SASTQTLSHL QGHLPSPWRP APTVTSASRR FIIKKNQKQS QNQNQKIQKEK 60
 TWGNGMRKRKG GEEGRRAGLW MHNSRARGLG RKIPQRPAAC VALARHVVFG GRLPIHPVEI120
 LVAGLLGGVK PVSDRQAGKG LGDGCCGRER V 151

(2) INFORMATION ON SEQ ID NO. 429:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

RHAGGGALGN LPPQPPGSGV MHPETCPSTF LASPLPHSIA PGLFLLDFVL VLALFLIFFY 60
 YESPGRGDS GSWPGPGRQV ALEMGXKLCR GAELSLCFSF FPLLLPLHTP VAGRNLGFPE120
 SLGVPPFLPH PGGTPRAPGL FLLLFSFWAV 150

(2) INFORMATION ON SEQ ID NO. 430:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 285 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

SWRTGGWAYA GDRLENKTSV SVASWASSLN ARMDNRFATA FVIACVLSLI STIYMAASIG 60
 TDEWYEYRSP VQENSSDLNK SIWDEFISDE ADEKTYNDAL FRYNGTVGLW RRCITIPKNM120
 HWYSPPERTE SFDVVTCKVS FTLTEQFMEK FVDLGNRNSG IDLLRTYLWR CQFLLPFVSL180
 GLMCFGALIG LCACICRSLY PTIATGILHL LAGLCTLGSV SCVAGIELL HQKLELPDNV240
 SGEGFWSFCL ACVSAPLQFM ASALTIWAH TNRKEYTLMK AYRVA 285

(2) INFORMATION ON SEQ ID NO. 431:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 116 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

LCPFWWAIPM HVFGYGDTPS PQSHCAIVSK KCIIIISLFIC LITNEFIPDA FIQITGIFLN 60
WTSIFIFPEVC ANGGCHVDDG NEAKHTSNYK CCSKTVIHSG IQTARPGCYG DRGLVL 116

Claims

1. A nucleic acid sequence that codes a gene product or a portion thereof, comprising

- a) a nucleic acid sequence, selected from the group Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, 391-403,

- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-127 and 391-403, or a complementary or allelic variant thereof.

3. Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403, characterized in that they are expressed elevated in normal bladder tissue.

4. BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 for use as vehicles for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has % homology to a human nucleic acid sequence.

7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a

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sufficient amount that they hybridize with the sequences according to claims 1 to 6.

8. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

15. A DNA fragment, comprising a gene, that can be obtained from the use according to claim 14.

16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to one of claims 16 or 17, wherein the prokaryotic cell system is *E. coli*, and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 16 to 18 are cultivated.

20. An antibody that is directed against a polypeptide or a fragment that is coded by the nucleic acids of sequences Seq. ID Nos. 1-127 and 391-403, which can be obtained according to claim 19.

21. An antibody according to claim , wherein it is monoclonal.

22. An antibody according to claim , wherein it is a phage display antibody.

23. Polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431.

24. Polypeptide partial sequences according to claim 23, with at least 80% homology to these sequences.

25. A polypeptide that is known from a phage display and that can bind to the polypeptide partial sequences according to claim 23.

26. Polypeptide partial sequences according to claim 23, with at least 90% homology to these sequences.
27. Use of polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431 as tools for finding active ingredients against the bladder tumor.
28. Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 for expression of polypeptides that can be used as tools for finding active ingredients against the bladder tumor.
29. Use of nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 in sense or antisense form.
30. Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 as pharmaceutical agents in gene therapy for treatment of the bladder tumor.
31. Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 for the production of a pharmaceutical agent for treatment of the bladder tumor.
32. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431.
33. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.
34. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.
35. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403.

36. Use of the genomic genes according to claim 33,
together with suitable regulatory elements.

37. Use according to claim 36, wherein the regulatory
element is a suitable promoter and/or enhancer.

38. A nucleic acid sequence according to claims 1 to 7,
wherein the size of the fragment has a length of at least 300 to
3500 bp.

Abstract

Human nucleic acid sequences -- mRNA, cDNA, genomic sequences -- from normal bladder tissue, which code for gene products or portions thereof, and their use, are described.

In addition, the polypeptides that can be obtained by way of the sequences and their use are described.

Systematic Gene Search in the Incyte LifeSeq Database

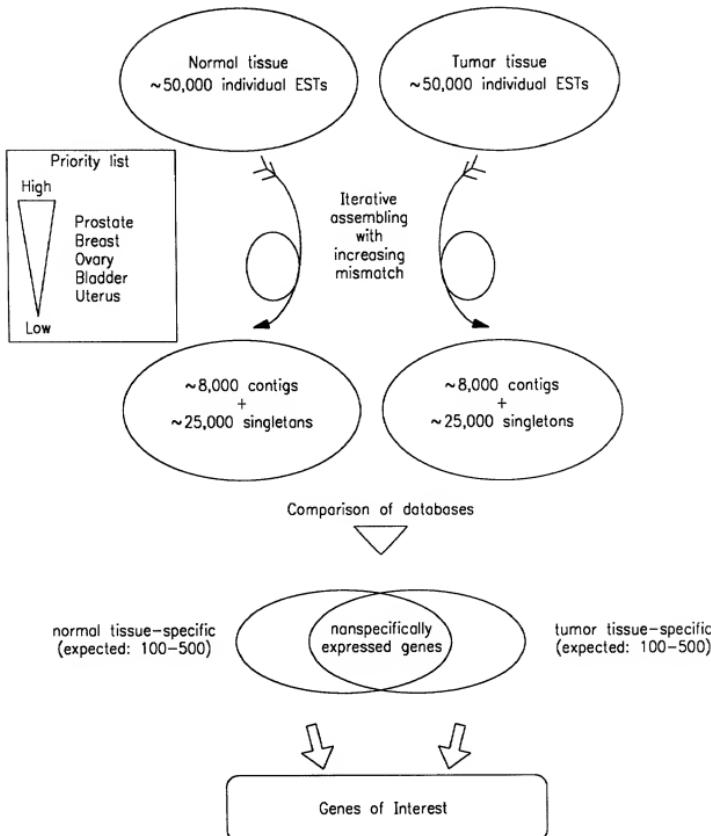
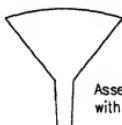


FIG. I

Principle of EST Assembly

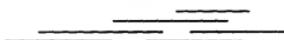
~50,000 ESTs per tissue



Assembly at 0% mismatch
with GAP4 (Staden)



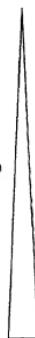
Contigs



Singletons



Contigs increasing in
number and length



Iterative assembly with
increasing mismatch
(1%, 2%, 4%)

5000–6000 Contigs ~25,000 other singlettons



~30,000 consensus-
sequences per tissue

FIG. 2a

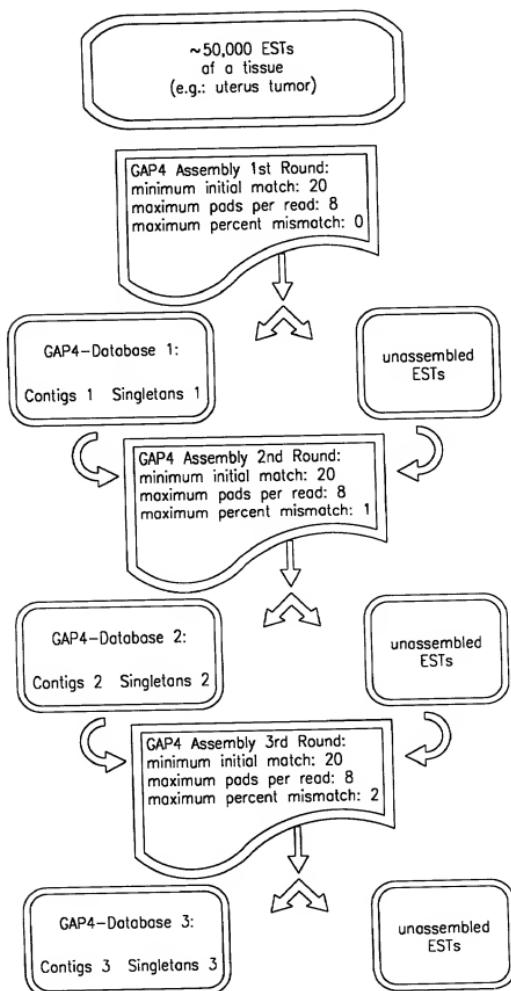


FIG. 2b-1

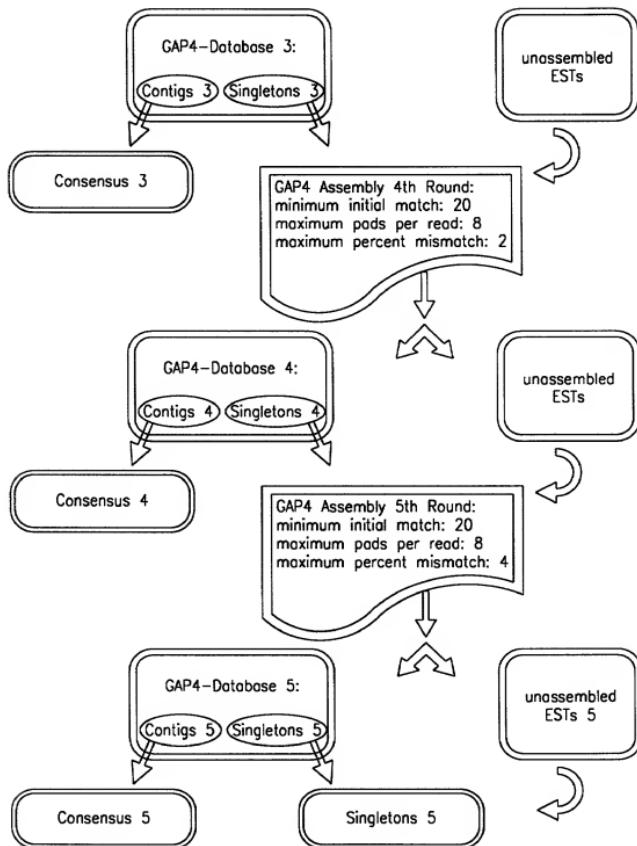


FIG. 2b-2

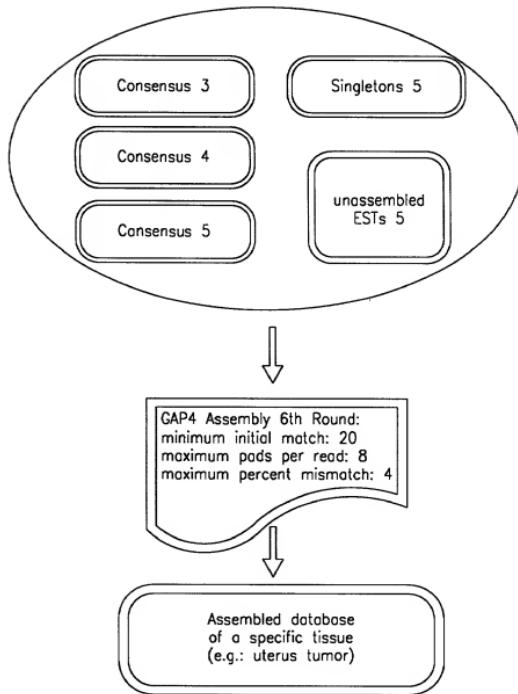


FIG. 2b-3

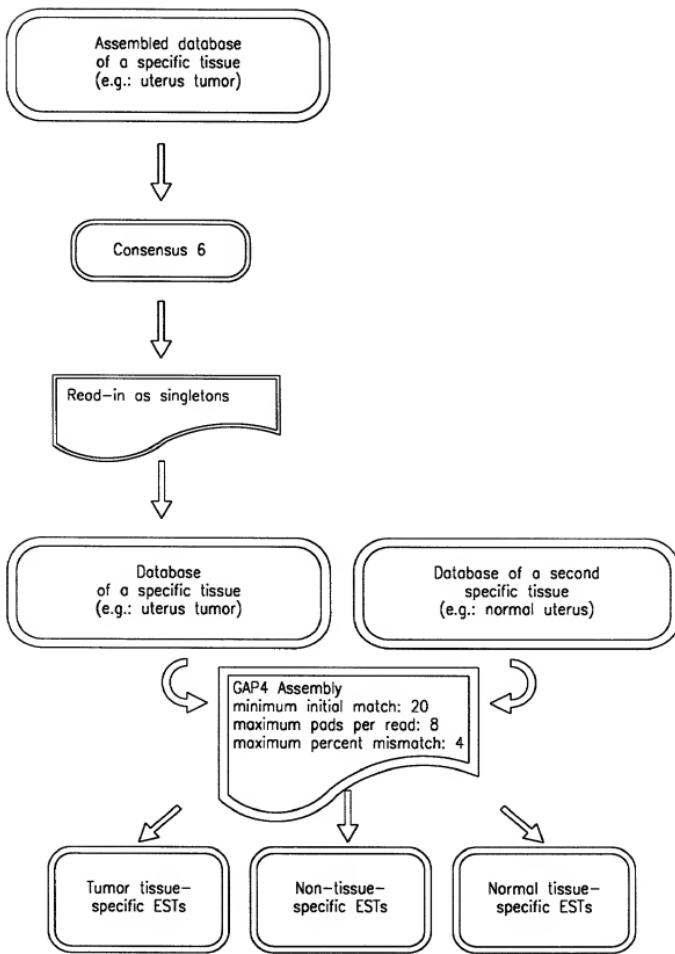


FIG. 2b-4

In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
cancer tissue

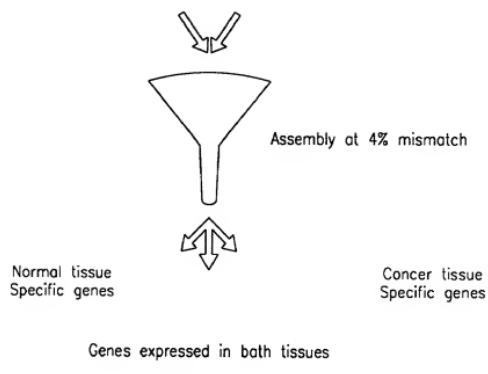


FIG. 3

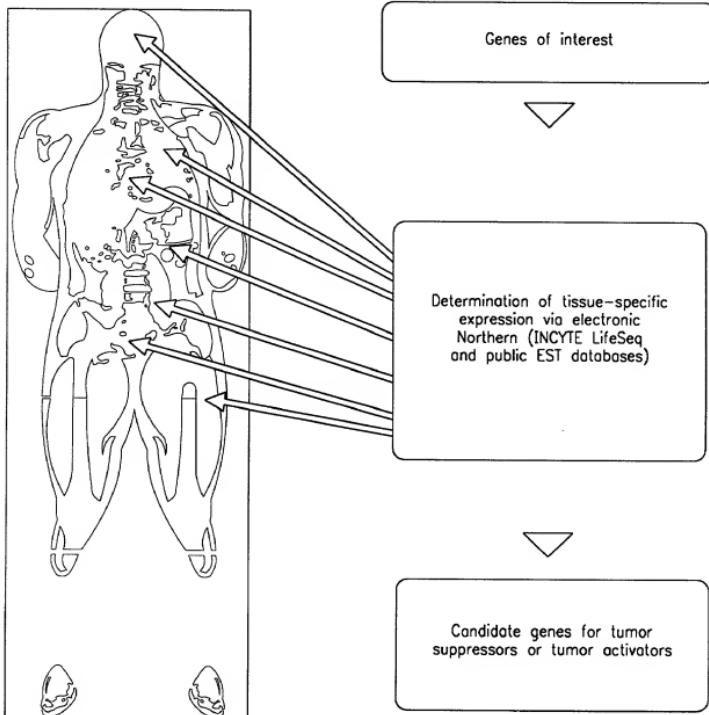


FIG. 4a

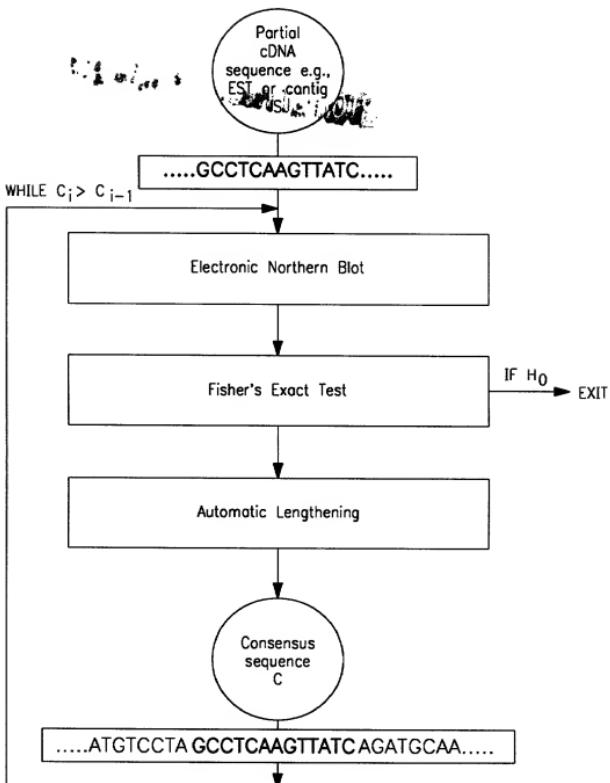
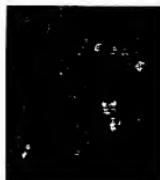


FIG. 4b

Isolation of genomic BAC and PAC clones

Chromosomal clone localization via FISH



Sequencing of clones that are located in regions that have chromosomal deletions in prostate and breast cancer leads to identification of candidate genes



Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues

FIG. 5

Attorney Docket Number: SCH 1781

DECLARATION FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

HUMAN NUCLEIC ACID SEQUENCES OF NORMAL BLADDER TISSUE

the specification of which

is attached hereto

was filed on 15 April 1999 as United States Application Number or PCT International Application Number PCT/DE99/01163 and (if applicable) was amended on _____

I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56.

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT international application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventors Certificate, or PCT International application having a filing date before that of the application on which priority is claimed.

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119

APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 18 620.7	Germany	21 April 1998	X

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)

APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120

APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,869); Alan E.J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brian P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Nancy J. Axelrod (44,014); James E. Ruian (40,921) and Jennifer J. Branigan (37,432).

Declaration for Patent Application (Continued)

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FAX (703) 243-6410

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full Name of sole or first inventor (given name, family name)

Thomas SPECHT

Signature

Date

24.10.00

Residence

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Citizenship

Germany

Post Office Address Grabenstrasse 14, D-12209 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

Bernd HINZMANN

Signature

Date

23.10.00

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Citizenship

Germany

Post Office Address Parkstrasse 19, D-13127 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

Armin SCHMITT

Signature

Date

Residence

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Citizenship

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Full Name of additional joint inventor (given name, family name)

Christian PILARSKY

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Full Name of additional joint inventor (given name, family name)

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Citizenship

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Full Name of additional joint inventor (given name, family name)

André ROSENTHAL

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Date

23.10.00

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Citizenship

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51587AW0MXX24-P

Attorney Docket Number: SCH 1781

DECLARATION FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

HUMAN NUCLEIC ACID SEQUENCES OF NORMAL BLADDER TISSUE

the specification of which

BT/

First
HJ

is attached hereto

was filed on 15 April 1999 as United States Application Number or PCT International Application Number PCT/DE99/01163 and (if applicable) was amended on _____

I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56.

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed.

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119			
APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 18 620.7	Germany	21 April 1998	X

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)	
APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120		
APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Alan E.J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brion P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,480); Nancy J. Axelrod (44,014); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

Declaration for Patent Application (Continued)

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 FAX (703) 243-6410

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full Name of sole or first inventor (given name family name)
--

Thomas SPECHT

Signature	Date
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Residence Berlin, Germany	Citizenship Germany
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Post Office Address Grabenstrasse 14, D-12209 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

Bernd HINZMANN

Signature	Date
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Residence Berlin, Germany	Citizenship Germany
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Full Name of additional joint inventor (given name, family name)

Armin SCHMITT

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